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(54) Title: FLOWERING TIME MODIFICATION

(57) Abstract: Recombinant polynucleotides and methods for modifying the flowering time of a plant are provided. Plants transformed with the recombinant polynucleotides may have flowering times that are accelerated, delayed or induced under specific conditions. Additionally, transformed plants may have altered vernalization requirements.

FLOWERING TIME MODIFICATION

The present invention claims priority in part from US Provisional Application Serial Nos. 60/159,464 filed October 12, 1999; 60/164,132 filed November 8, 1999; 60/166,228 filed November 17, 1999; 60/197,899 filed April 17, 2000; and Plant Trait Modification III, filed August 22, 2000.

FIELD OF THE INVENTION

This invention is in the field of plant molecular biology and relates to compositions and methods for modifying a plant's flowering time or vernalization requirements.

BACKGROUND OF THE INVENTION

In order to maximize reproductive success, plants have evolved complex mechanisms to ensure that flowering occurs under favorable conditions. Analysis of late flowering mutants and ecotypes in *Arabidopsis* has revealed that such mechanisms are based upon several genetic pathways which may contain 80 or more genes (Martinez-Zapater and Somerville, (1990) *Plant Physiol.* 92:770-776; Koornneef et al. (1991) *Mol. Gen. Genet.* 229:57-66; EM Meyerwitz and CR Somerville Eds (1994) *Arabidopsis* pp 403-433 Cold Spring Harbor Laboratory Press, New York). Together these loci co-ordinate flowering time with environmental variables (e.g. day-length, temperature, light quality, and nutrient availability) and with the developmental stage of the plant.

Arabidopsis flowers rapidly when grown under long day conditions of 16 hours or continuous light, but flowers much later under short day conditions of 8 or 10 hours light. Genes regulating this response constitute the photoperiod pathway and were identified by mutations that cause late flowering under long day conditions but which do not alter flowering in short day conditions. Examples from this group, which promote flowering in response to long days, include *CONSTANS* (CO), *GIGANTEA* (GI), *FT*, *FWA*, *FE*, *FD*, and *FHA*. A second group of genes, which includes *LUMINIDEPENDENS* (LD), *FCA*, *FVE*, *FY*, and *FPA*, form an autonomous pathway that is active under all day-length conditions. Mutants for this second class of genes flower later than wild type controls irrespective of the day length conditions (Koornneef et al. (1991) *Mol. Gen. Genet.* 229:57-66; EM Meyerwitz and CR Somerville Eds (1994) *Arabidopsis* pp 403-433 Cold Spring Harbor Laboratory Press, New York).

In addition to differing in their response to day-length, mutants from the photoperiod and autonomous pathways show a differential response to prolonged cold (vernalization) treatments (Vince-Prue, (1975) *Vernalization*. In *Photoperiodism in Plants* pp 263-291, McGraw Hill, London) Through a vernalization response, *Arabidopsis* ecotypes from Northern

latitudes, such as Stockholm, are adapted to flower in the spring following exposure to cold winter conditions. This avoids flowering in the late summer when seed maturation might be curtailed by the onset of winter conditions (Reeves and Coupland, (2000) *Curr. Opin. Plant Biol* 3:37-42). When these ecotypes are grown in the laboratory they flower late, but will flower much earlier if subjected to a cold period of 4-6 weeks during seed germination. In a comparable manner, mutants from the autonomous pathway exhibit a very marked reduction in flowering time when subjected to vernalization. In contrast, mutants from the photoperiod pathway only show a minor response to cold treatments (Chandler *et al.*, (1996) *Plant J.* 10:637-644; Koornneef *et al.*, (1998) *Genetics* 148:885-892). Thus, vernalization can overcome the requirement for the autonomous pathway conditions (Reeves and Coupland, (2000) *Curr. Opin. Plant Biol* 3:37-42).

Two *Arabidopsis* genes, *FLOWERING LOCUS C*, *FLC* (also known as *FLOWERING LOCUS F*, *FLF*) and *FRIGIDA* (*FRI*), act in conjunction to repress flowering in the absence of a vernalization treatment (Napp-Zinn, K. (1957) *Indukt. Abstammungs. Verebungsl.* 88:253-285; Napp-Zinn K. (1985) *CRC Handbook of Flowering*, Vol. 1, A. H. Halevy, pp 492-503; Clarke and Dean (1994) *Mol. Gen. Genet.* 248:81-89; Koornneef. *et al.*, (1994) *Plant Journal* 6:911-919; Lee *et al.*, (1994) *Plant Journal* 6:903-909.) Dominant functional alleles of *FLC* and *FRI* are found together in Northern European *Arabidopsis* ecotypes such as Pitztal and Stockholm. These ecotypes are extremely late flowering when non-vernalized. The widely used laboratory ecotype Columbia contains functional alleles at only one of these two loci and flower slightly later than strains such as Landsberg *erecta* which possess functional alleles of neither gene. The *FRIGIDA* protein sequence has not yet been published. However, the *FLC* gene has recently been cloned and shown to encode a MADS box protein (Sheldon C. *et al.*, 1999, *Plant Cell* 11:445-458; Michaels S. and Amasino, R., 1999, *Plant Cell* 11:949-956). Dominant alleles and overexpression of *FLC* have been reported to delay flowering, while null *flc* mutants are early flowering (Lee *et al.*, (1994) *Plant J.* 6:903-909; Michaels and Amasino, (1999) *Plant Cell* 11:949-956; Sheldon *et al.*, (1999) *Proc. Natl. Acad. Sci.* 97:3753-3758). Thus, *FLC* acts to prevent premature flowering.

We have discovered transcription factors that regulate flowering time or vernalization requirements of plants. These transcription factors could therefore be useful to manipulate flowering characteristics of a plant.

SUMMARY OF THE INVENTION

In one aspect, the present invention relates to a transgenic plant comprising a recombinant polynucleotide. The recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a

sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28 but excluding SEQ ID No. 28, and the presence of the recombinant polynucleotide alters the flowering time or vernalization requirements of the transgenic plant when compared with the same trait of another plant lacking the recombinant polynucleotide.

5 In one embodiment, the nucleotide sequence encodes a polypeptide comprising a conserved domain such as 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA binding domain of SEQ ID Nos. 2N, where N=1-28. In another embodiment, the recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence
10 selected from the group consisting of SEQ ID Nos. 2N, where N=1-28. In a further embodiment, the nucleotide sequence further comprises a promoter operably linked to the nucleotide sequence. The promoter may be a constitutive or inducible or tissue-active.

 In a second aspect, the present invention relates to a method for altering a plant's flowering time or vernalization requirements. The method comprises (a) transforming a plant
15 with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28; (b) selecting transformed plants; and (c) identifying a transformed plant with the desired trait.

 In one embodiment, the nucleotide sequence encodes a polypeptide comprising a
20 conserved domain such as 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA binding domain domain of SEQ ID Nos. 2N, where N=1-28 but excluding SEQ ID No. 28. In another embodiment, the recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2N,
25 where N=1-28. In a further embodiment, the nucleotide sequence further comprises a promoter operably linked to the nucleotide sequence. The promoter may be a constitutive or inducible or tissue-active.

 In a third aspect, the present invention relates to another method for altering a plant trait associated with flowering time or the plant's vernalization requirements. The method
30 comprises (a) transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence comprising at least 18 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-28 but excluding SEQ ID No. 27; and (b) selecting said transformed plant.

 In yet another aspect, the present invention is yet another method for altering a plant's
35 flowering time or vernalization requirements. The method comprises (a) providing a database sequence; (b) comparing the database sequence with a polypeptide selected from SEQ ID Nos. 2N, where N= 1-28; (c) selecting a database sequence that meets selected sequence

criteria; and (d) transforming said database sequence in the plant. Alternatively, the database sequence can be compared with a polynucleotide selected from SEQ ID Nos. 2N-1, where N= 1-28.

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BRIEF DESCRIPTION OF THE FIGURES

Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 2 provides a table of sequences that are homologous to the sequences provided in the Sequence Listing. The table includes from left to right: the SEQ ID No., the internal code reference number, the unique Genbank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

A "recombinant polynucleotide" is a nucleotide sequence comprising a gene coding sequence or a fragment thereof (comprising at least 18 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 50 consecutive nucleotides). Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker or the like. The polynucleotide may comprise single stranded or double stranded DNA or RNA. The polynucleotide may comprise modified bases or a modified backbone. The polynucleotide may be genomic, a transcript (such as an mRNA) or a processed nucleotide sequence (such as a cDNA). The polynucleotide may comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide is comprised of a nucleotide sequence not found in nature or the polynucleotide is separated from nucleotide sequences with which it typically is in proximity or is next to nucleotide sequences with which it typically is not in proximity.

A "recombinant polypeptide" is a polypeptide derived from the translation of a recombinant polynucleotide or is more enriched in a cell than the polypeptide in its natural

state in a wild type cell, e.g. more than 5% enriched, more than 10% enriched or more than 20% enriched and is not the result of a natural response of a wild type plant or is separated from other components with which it is typically associated with in a cell.

5 A "transgenic plant" may refer to a plant that contains genetic material not normally found in a wild type plant of the same species, or in a naturally occurring variety or in a cultivar, and which has been introduced into the plant by human manipulation. A transgenic plant is a plant that may contain an expression vector or cassette. The expression cassette comprises a gene coding sequence and allows for the expression of the gene coding sequence. The expression cassette may be introduced into a plant by transformation or by
10 breeding after transformation of a parent plant.

A transgenic plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells, protoplasts or any other plant material, and progeny thereof.

The phrase "altered expression" in reference to polynucleotide or polypeptide
15 expression refers to an expression pattern in the transgenic plant that is different from the expression pattern in the wild type plant or a reference; for example, by expression in a cell type other than a cell type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at
20 different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern may be transient or stable, constitutive or inducible.

A "transcription factor" (TF) refers to a polynucleotide or polypeptide that controls the
25 expression of a gene or genes either directly by binding to one or more nucleotide sequences associated with a gene coding sequence or indirectly by affecting the level or activity of other polypeptides that do bind directly or indirectly to one or more nucleotide sequences associated with a gene coding sequence. A TF, in this definition, includes any polypeptide that can activate or repress transcription of a single gene or a number of genes. This polypeptide
30 group includes, but is not limited to, DNA binding proteins, protein kinases, protein phosphatases, GTP-binding proteins and receptors.

The transcription factor sequence may comprise a whole coding sequence or a fragment or domain of a coding sequence. A "fragment or domain", as referred to
35 polypeptides, may be a portion of a polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner or to a similar extent as does the intact polypeptide. A fragment may comprise, for example, a DNA binding domain that binds to a specific DNA promoter region, an activation domain or a domain for protein-protein

interactions. Fragments may vary in size from as few as 6 amino acids to the length of the intact polypeptide, but are preferably at least 30 amino acids in length and more preferably at least 60 amino acids in length. In reference to a nucleotide sequence "a fragment" refers to any sequence of at least consecutive 18 nucleotides, preferably at least 30 nucleotides, more preferably at least 50, of any of the sequences provided herein.

Exemplary polynucleotides and polypeptides comprise a sequence provided in the Sequence Listing as SEQ ID No. 1: G157 (cDNA); SEQ ID No. 2: G157 (protein); SEQ ID No. 3: G859 (cDNA); SEQ ID No. 4: G859 (protein); SEQ ID No. 5: G859.1 (cDNA); SEQ ID No. 6: G859.1 (protein); SEQ ID No. 7: G859.2 (cDNA); SEQ ID No. 8: G859.2 (protein); SEQ ID No. 9: G1842 (cDNA); SEQ ID No. 10: G1842 (protein); SEQ ID No. 11: G1842.2 (cDNA); SEQ ID No. 12: G1842.2 (protein); SEQ ID No. 13: G1842.6 (cDNA); SEQ ID No. 14: G1842.6 (protein); SEQ ID No. 15: G1842.7 (cDNA); SEQ ID No. 16: G1842.7 (protein); SEQ ID No. 17: G1843 (cDNA); SEQ ID No. 18: G1843 (protein); SEQ ID No. 19: G1844 (cDNA); SEQ ID No. 20: G1844 (protein); SEQ ID No. 21: G1844.2 (cDNA); SEQ ID No. 22: G1844.2 (protein); SEQ ID No. 23: G861 (cDNA); SEQ ID No. 24: G861 (protein); SEQ ID No. 25: G861.1 (cDNA); SEQ ID No. 26: G861.1 (protein); SEQ ID No. 27: G1759 (cDNA); SEQ ID No. 28: G1759 (protein); SEQ ID No. 29: G192 (cDNA); SEQ ID No. 30: G192 (protein); SEQ ID No. 31: G234 (cDNA); SEQ ID No. 32: G234 (protein); SEQ ID No. 33: G361 (cDNA); SEQ ID No. 34: G361 (protein); SEQ ID No. 35: G486 (cDNA); SEQ ID No. 36: G486 (protein); SEQ ID No. 37: G748 (cDNA); SEQ ID No. 38: G748 (protein); SEQ ID No. 39: G994 (cDNA); SEQ ID No. 40: G994 (protein); SEQ ID No. 41: G1335 (cDNA); SEQ ID No. 42: G1335 (protein); SEQ ID No. 43: G562 (cDNA); SEQ ID No. 44: G562 (protein); SEQ ID No. 45: G736 (cDNA); SEQ ID No. 46: G736 (protein); SEQ ID No. 47: G1073 (cDNA); SEQ ID No. 48: G1073 (protein); SEQ ID No. 49: G1435 (cDNA); SEQ ID No. 50: G1435 (protein); SEQ ID No. 51: G180 (cDNA); SEQ ID No. 52: G180 (protein); SEQ ID No. 53: G592 (cDNA); SEQ ID No. 54: G592 (protein); SEQ ID No. 55: G208 (cDNA); and SEQ ID No. 56: G208 (protein).

A "conserved domain" refers to a polynucleotide or polypeptide fragment that is more conserved at a sequence level than other fragments when the polynucleotide or polypeptide is compared with homologous genes or proteins from other plants. The conserved domain may be 1) a localization domain, 2) an activation domain, 3) a repression domain, 4) a dimerization or oligomerization domain, 5) a DNA binding domain or any combination thereof. For MADS proteins, the conserved domain is typically a DNA-binding domain.

A nucleotide sequence is "operably linked" when it is placed into a functional relationship with another nucleotide sequence. For example, a promoter or enhancer is operably linked to a gene coding sequence if the presence of the promoter or enhancer increases the level of expression of the gene coding sequence.

“Trait” refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. This characteristic may be visible to the human eye, such as seed or plant size, or be measured by biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes by employing Northern, RT PCR, microarray gene expression assays or reporter gene expression systems or be measured by agricultural observations such as stress tolerance, yield or disease resistance.

“Trait modification” refers to a detectable difference in a characteristic in a transgenic plant with modified expression of a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. The trait modification may entail at least a 5% increase or decrease in an observed trait (difference), at least a 10% difference, at least a 20% difference, at least a 30%, at least a 50%, at least a 70%, at least a 100% or a greater difference. It is known that there may be a natural variation in the modified trait. Therefore, the trait modification observed entails a change in the normal distribution of the trait in transgenic plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (embryo), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; enhanced resistance to microbial, fungal or viral diseases; resistance to nematodes, decreased herbicide sensitivity, enhanced tolerance of heavy metals (or enhanced ability to take up heavy metals), enhanced growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotypes that may be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenolipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that may be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that may be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

Of particular interest are traits relating to modified vernalization requirements or flowering time characteristics, such as changes in flowering time in response to day-length, in response to temperature, in response to light quality, nutrient availability, and development stage of the plant, and the like.

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1. The Sequences

We have discovered particular plant transcription factors (TFs) that can be employed to modify the flowering time of a plant. Therefore, the flowering time of plants can be either decreased, increased, or made inducible under specific conditions using the TFs of this invention. Additionally, the transcription factors can be used to modify the vernalization requirements of the plant.

The plant transcription factors may belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4:1575-1588); the zinc finger protein (Z) family (Klug and Schwabe (1995) *FASEB J.* 9: 597-604); the homeobox (HB) protein family (Duboule (1994) *Guidebook to the Homeobox Genes*, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) *Mol. Gen. Genet.* 1996 250:7-16); the NAM protein family (Souer et al. (1996) *Cell* 85:159-170); the IAA/AUX proteins (Rouse et al. (1998) *Science* 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8:192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) *Plant J.* 4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl. Acids Res. Mol. Biol.* 54:35-100); the scarecrow (SCR) family (Di Laurenzio et al. (1996) *Cell* 86:423-433); the GF14 family (Wu et al. (1997) *Plant Physiol.* 114:1421-1431); the polycomb (PCOMB) family (Kennison (1995) *Annu. Rev. Genet.* 29:289-303); the teosinte branched (TEO) family (Luo et al. (1996) *Nature* 383:794-799); the ABI3 family (Giraudat et al. (1992) *Plant Cell* 4:1251-1261); the triple helix (TH) family (Dehesh et al. (1990) *Science* 250:1397-1399); the EIL family (Chao et al. (1997) *Cell* 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) *Journal of Biological Chemistry* 265:8573-8582); the S1FA family (Zhou et al. (1995) *Nucleic Acids Res.* 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109:723); the YABBY family (Bowman et al. (1999) *Development* 126:2387-96); the PAZ family (Bohmert et al. (1998)

EMBO J. 17:170-80); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) *Plant J.* 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the golden (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936), and the TUBBY family (Boggin et al, (1999) *Science* 286:2119-2125)

5 In particular, the TFs that we have discovered that are implicated in flowering time or vernalization include members of the MADS transcription factor family, the MYB family, the WRKY family, the HLH/MYC family, GLD family, AT-HOOK family, the CAAT family, the bZIP family, and members of zinc coordinating protein families (Z-Dof, Z-CLDSH and Z-CH2H2). In fact we have identified the first members of the WRKY, CAAT, bZIP, AT-HOOK and HLH/MYC
10 families that are associated with flowering time modification in plants: G192 and G190 (WRKY), G486 (CAAT), G562 (bZIP), G1073 (AT-HOOK) and G592 (HLH/MYC).

The polynucleotides and polypeptides are provided in the Sequence Listing and are tabulated in Figure 1. Figure 1 identifies a SEQ ID No., its corresponding GID number, whether the sequence is a polynucleotide or a polypeptide sequence, and indicates the
15 conserved domains. We have also identified domains or fragments derived from each of the sequences in the Sequence Listing. The fragments can be from any region of the sequence, can be of any length up to the length of the sequence, and can be as short as six residues for protein and 18 nucleotides for DNA. Exemplary fragments of the DNA sequences are as follows: 1-50, 51-100, 101-200, 201-218, 218-300, 301-450 and 450-600; and exemplary
20 fragments of proteins are as follows 1-50, 51-100, 101-200, 201-206, 206-250, 251-300. For DNA sequences, the numbers may be measured from either 5' or 3' end of the DNA. For the protein sequences the fragment location is determined from the N-terminus or C-terminus of the protein and may include adjacent amino acid sequences, such as for example for SEQ ID No. 2 an additional 10, 20, 40, 60 or 100 amino acids in either N-terminal or C-terminal
25 direction of the described fragments.

The identified polypeptide fragments may be linked to fragments or sequences derived from other transcription factors so as to generate additional novel sequences, such as by employing the methods described in Short, PCT publication WO9827230, entitled "Methods and Compositions for Polypeptide Engineering" or in Patten et al., PCT publication
30 WO9923236, entitled "Method of DNA Shuffling" or in Minshull and Stemmer, US Patent No. 5,837,458. Alternatively, the identified fragment may be linked to a transcription activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. A common feature of some activation domains is that they are designed to form amphiphilic alpha helices with excess positive or negative charge (Giniger and Ptashne (1987) *Nature* 330:670-672, Gill and Ptashne (1987) *Cell* 51:121-126, Estruch et al (1994) *Nucl. Acids Res.* 22:3983-3989). Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) *Proc. Natl. Acad. Sci. USA* 95: 376-381; and Aoyama et al.
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(1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, supra).

The isolated polynucleotides and polypeptides may be used to modify plant development, physiology or biochemistry such that the modified plants have a trait advantage over wild type plants. The identified polynucleotide fragments are also useful as nucleic acid probes and primers. A nucleic acid probe is useful in hybridization protocols, including protocols for microarray experiments. Primers may be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York (1989) and Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

2. Identification of Homologous Sequences (Homologs)

Homologous sequences to those provided in the Sequence Listing derived from *Arabidopsis thaliana* or from other plants may be used to modify a plant trait. Homologous sequences may be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype may be changed include barley, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, sweet potato and beans. The homologs may also be derived from woody species, such pine, poplar and eucalyptus.

Substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) *Meth. Enzymol.* (1993) vol. 217, Academic Press). Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are

made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues.

Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure.

Substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions may be conservative with little effect on the function of the gene, for example by substituting alanines for serines, arginines for lysines, glutamate for aspartate and the like. The substitutions which are not conservative are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Additionally, the term "homologous sequence" may encompass a polypeptide sequence that is modified by chemical or enzymatic means. The homologous sequence may be a sequence modified by lipids, sugars, peptides, organic or inorganic compounds, by the use of modified amino acids or the like. Protein modification techniques are illustrated in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

Homologous sequences also may mean two sequences having a substantial percentage of sequence identity after alignment as determined by using sequence analysis programs for database searching and sequence alignment and comparison available, for example, from the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) may be searched. Alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window may be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous

positions. A description of the method is provided in Ausubel et al. (eds) (1999) *Current Protocols in Molecular Biology*, John Wiley & Sons.

Transcription factors that are homologs of the disclosed sequences will typically share at least 40% amino acid sequence identity. More closely related TFs may share at least 50%,
5 60%, 65%, 70%, 75% or 80% sequence identity with the disclosed sequences. Factors that are most closely related to the disclosed sequences share at least 85%, 90% or 95% sequence identity. At the nucleotide level, the sequences will typically share at least 40% nucleotide sequence identity, preferably at least 50%, 60%, 70% or 80% sequence identity, and more preferably 85%, 90%, 95% or 97% sequence identity. The degeneracy of the
10 genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein.

One way to identify whether two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific
15 sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Conditions for nucleic acid hybridization and calculation of stringencies can be found in Sambrook et al. (1989) *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York and Tijssen (1993) *Laboratory Techniques in Biochemistry and
20 Molecular Biology--Hybridization with Nucleic Acid Probes* Part I, Elsevier, New York. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For detecting less closely related homologs washes may be performed at 50° C.

For conventional hybridization the hybridization probe is conjugated with a detectable label such as a radioactive label, and the probe is preferably of at least 20 nucleotides in length. As is well known in the art, increasing the length of hybridization probes tends to give enhanced specificity. The labeled probe derived from the *Arabidopsis* nucleotide sequence may be hybridized to a plant cDNA or genomic library and the hybridization signal detected
30 using means known in the art. The hybridizing colony or plaque (depending on the type of library used) is then purified and the cloned sequence contained in that colony or plaque isolated and characterized. Homologs may also be identified by PCR-based techniques, such as inverse PCR or RACE, using degenerate primers. See Ausubel et al. (eds) (1998) *Current Protocols in Molecular Biology*, John Wiley & Sons.

35 TF homologs may alternatively be obtained by immunoscreening an expression library. With the provision herein of the disclosed TF nucleic acid sequences, the polypeptide may be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise

antibodies (monoclonal or polyclonal) specific for the TF. Antibodies may also be raised against synthetic peptides derived from TF amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone the TF homolog, using the methods described above. The selected cDNAs may be confirmed by sequencing and biological activity.

3. Altered Expression of Transcription Factors

Any of the identified sequences may be incorporated into a cassette or vector for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) *Methods for Plant Molecular Biology*, Academic Press, and Gelvin et al., (1990) *Plant Molecular Biology Manual*, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella, L., et al., (1983) *Nature* 303: 209, Bevan, M., *Nucl. Acids Res.* (1984) 12: 8711-8721, Klee, H. J., (1985) *Bio/Technology* 3: 637-642, for dicotyledonous plants. Ti-derived plasmids can be transferred into both monocotyledonous and dicotyledonous species using *Agrobacterium*-mediated transformation (Ishida et al (1996) *Nat. Biotechnol.* 14:745-50; Barton et al. (1983) *Cell* 32:1033-1043).

Alternatively, non-Ti vectors can be used to transfer the DNA into plants and cells by using free DNA delivery techniques. Such methods may involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou, P., (1991) *Bio/Technology* 9: 957-962) and corn (Gordon-Kamm, W., (1990) *Plant Cell* 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks, T. et al., (1993) *Plant Physiol.* 102: 1077-1084; Vasil, V., (1993) *Bio/Technology* 10: 667-674; Wan, Y. and Lemeaux, P., (1994) *Plant Physiol.* 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al., (1996) *Nature Biotech.* 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequences (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which may be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (see, e.g., Odel et al., (1985) *Nature* 313:810); the nopaline synthase promoter (An et al., (1988) *Plant Physiol.* 88:547); and the octopine synthase promoter (Fromm et al., (1989) *Plant Cell* 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of the TFs in plants, as illustrated by seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186; fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) *Plant Mol. Biol.* 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) *Plant Mol. Biol.* 37:977-988), flower-specific (Kaiser et al. (1995) *Plant Mol. Biol.* 28:231-243), pollen (Baerson et al. (1994) *Plant Mol. Biol.* 26:1947-1959), carpels (Ohl et al. (1990) *Plant Cell* 2:837-848), pollen and ovules (Baerson et al. (1993) *Plant Mol. Biol.* 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al (1999) *Plant Mol. Biol.* 39:979-990 or Baumann et al. (1999) *Plant Cell* 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) *Plant Mol. Biol.* 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) *Plant Mol. Biol.* 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley, et al. (1993) *Plant Mol. Biol.* 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al., (1989) *Plant Cell* 1:471, and the maize rbcS promoter, Schaffner and Sheen, (1991) *Plant Cell* 3: 997); wounding (e.g., *wun1*, Siebertz et al., (1989) *Plant Cell* 1: 961); pathogen resistance, and chemicals such as methyl jasmonate or salicylic acid. (Gatz et al., (1997) *Plant Mol. Biol.* 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at late seed development (Odell et al. (1994) *Plant Physiol.* 106:447-458).

Plant expression vectors may also include RNA processing signals that may be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors may include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Finally, as noted above, plant expression vectors may also include dominant selectable marker genes to allow for the ready selection of transformants. Such genes include those encoding antibiotic resistance genes (e.g., resistance to hygromycin, kanamycin, bleomycin, G418, streptomycin or spectinomycin) and herbicide resistance genes (e.g., phosphinothricin acetyltransferase).

A reduction of TF expression in a transgenic plant to modify a plant trait may be obtained by introducing into plants antisense constructs based on the TF cDNA. For antisense suppression, the TF cDNA is arranged in reverse orientation relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length TF cDNA or gene, and need not be identical to the TF cDNA or a gene found in the plant type to be transformed. Generally, however, where the introduced sequence is of shorter length, a higher degree of homology to the native TF sequence will be needed for effective antisense suppression. Preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous TF gene in the plant cell. Suppression of endogenous TF gene expression can also be achieved using a ribozyme. Ribozymes are synthetic RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 to Cech and U.S. Patent No. 5,543,508 to Haselhoff. The inclusion of ribozyme sequences within antisense RNAs may be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that bind to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by the TF cDNA (or variants thereof) is over-expressed may also be used to obtain co-suppression of the endogenous TF gene in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire TF cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous TF gene. However, as with antisense suppression, the suppressive efficiency will be enhanced as (1) the introduced sequence is lengthened and (2) the sequence similarity between the introduced sequence and the endogenous TF gene is increased.

Vectors expressing an untranslatable form of the TF mRNA may also be used to suppress the expression of endogenous TF activity to modify a trait. Methods for producing such constructs are described in U.S. Patent No. 5,583,021 to Dougherty et al. Preferably, such constructs are made by introducing a premature stop codon into the TF gene. Alternatively, a

plant trait may be modified by gene silencing using double-strand RNA (Sharp (1999) *Genes and Development* 13: 139-141). This approach, whereby a vector is prepared in which a cDNA or gene is arranged in duplicated fashion and is capable of generating upon expression a double stranded RNA molecule with a hairpin structure. This procedure has been used to modify gene activity in plants (Chuang and Meyerowitz (1999) *Proc. Natl. Acad. Sci.* 97:4985-9490).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a TF gene. Mutants containing a single mutation event at the desired gene may be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) *Methods in Arabidopsis Research*. World Scientific).

A plant trait may also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome may be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention may also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al., (1997) *Nature* 390 698-701, Kakimoto et al., (1996) *Science* 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant may be modified so as to increase transcription levels of a polynucleotide of the invention (See PCT Publications WO9606166 and WO 9853057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant may also comprise the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

4. Transgenic Plants with Modified TF Expression

Once an expression cassette comprising a polynucleotide encoding a TF gene of this invention has been constructed, standard techniques may be used to introduce the polynucleotide into a plant in order to modify a trait of the plant. The plant may be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae*

(melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) *Handbook of Plant Cell Culture –Crop Species*. Macmillan Publ. Co. Shimamoto et al. (1989) *Nature* 338:274-276; Fromm et al. (1990) *Bio/Technology* 8:833-839; and Vasil et al. (1990) *Bio/Technology* 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods may include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait may be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention may be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

5. Commercial Applications of the Polynucleotides and Polypeptides

Specific applications for the genes of the present invention relate to their potential roles in plant flowering time or the vernalization response. Most modern crop varieties are the result of extensive breeding programs and many generations of backcrossing may be required

to introduce desired traits. Systems that accelerate flowering could have valuable applications in such programs since they allow much faster generation times. Additionally, in some instances, a faster generation time might allow additional harvests of a crop to be made within a given growing season. With the advent of transformation systems for tree species such as oil palm, aspen, pine and eucalyptus, forest biotechnology is a growing area of interest.

Also, in species such as sugarbeet where the vegetative parts of the plants constitute the crop and the reproductive tissues are discarded, it would be advantageous to delay or prevent flowering. Extending vegetative development could bring about large increases in yields.

Furthermore, by regulating the expression of flowering-time controlling genes, using inducible promoters, flowering could potentially be triggered as desired (for example, by application of a chemical inducer). This would allow, for example, flowering to be synchronized across a crop and facilitate more efficient harvesting. Such inducible systems could be used to tune the flowering of crop varieties to different latitudes. At present, species such as soybean and cotton are available as a series of maturity groups that are suitable for different latitudes on the basis of their flowering time (which is governed by day-length). A system in which flowering could be chemically controlled would allow a single high-yielding northern maturity group to be grown at any latitude. In southern regions such plants could be grown for longer, thereby increasing yields, before flowering was induced. In more northern areas, the induction would be used to ensure that the crop flowers prior to the first winter frosts. Currently, the existence of a series of maturity groups for different latitudes represents a major barrier to the introduction of new valuable traits.

For many crop species, high yielding winter-varieties can only be grown in temperate regions where the winter season is prolonged and cold enough to elicit a vernalization response. Altered expression of the genes of the invention could compensate for a vernalization treatment in late-flowering *Arabidopsis* ecotypes. Similar effects might be achieved in crop plants. Winter varieties of wheat, for instance, which over-express G157 (or the wheat ortholog) might then be grown in areas like Southern California which would otherwise be too warm to allow effective vernalization. A second application for this system is in cherry (*Prunus*). Locally grown cherries are unavailable in the early Californian spring since the winters are too warm for vernalization to occur.

A further application exists in strawberry (*Fragaria*). Strawberry has a well-defined perennial cycle of flower initiation, dormancy, chilling, crop growth and runner production. In temperate European countries, the plants flower in early spring, and fruit is produced in May or June. Following fruiting, runners are generated that carry plantlets which take root. The plants then remain dormant all through the late summer and autumn. Flowering cannot be repeated until the following spring after the plants have received a winter cold treatment. A

system, which bypasses this vernalization requirement, might permit a second autumn crop of strawberries to be harvested in addition to the spring crop.

Finally, in addition to the direct applications of the genes themselves, their regulatory regions could also be of value. If the promoters of these genes are responsive to low temperatures they could be incorporated into expression systems for regulation of genes that confer tolerance to freezing. Such genes would then be up regulated specifically at the time required, thereby minimizing any toxic effects that result from their constitutive expression.

6. Other Utility of the Polypeptide and Polynucleotides

A transcription factor coding provided by the present invention may also be used to identify exogenous or endogenous molecules that may affect expression of the transcription factors and may affect flowering time. These molecules may include organic or inorganic compounds.

For example, the method may entail first placing the molecule in contact with a plant or plant cell. The molecule may be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide may be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence may be detected by use of microarrays, Northern's or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998). Such changes in the expression levels may be correlated with modified plant traits and thus identified molecules may be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

The transcription factors may also be employed to identify promoter sequences with which they may interact. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence may be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences may be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the TFs with their promoters (Bulyk et al. (1999) *Nature Biotechnology* 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification may occur by covalent modification, such

as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions may be employed. Among the methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

5 The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), *Proc. Natl. Acad. Sci. USA*, 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's
10 activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of
15 the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After
20 identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions may be preformed.

 The following examples are intended to illustrate but not limit the present invention.

EXAMPLES

Methods

25 All experiments were performed using *Arabidopsis* of ecotype Columbia except where otherwise indicated. The Stockholm (CS6863) and Pitztal (CS6832) lines were supplied by the ABRC at Ohio State University. In all experiments, seeds were sterilized by a 2 minute ethanol treatment followed by 30 minutes in 30% bleach / 0.01% Tween and five washes in distilled water. Seeds were sown to MS agar in 0.1% agarose and stratified for 3-5 days at 4
30 °C, before transfer to growth rooms with a temperature of 20-25 °C. MS media was supplemented with 50mg/l kanamycin for selection of transformed plants. Plants were transplanted to soil after 7 days of growth on plates. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside
35 plates containing freshly sown non-vernalized controls. Whole vegetative seedlings were harvested for gene expression analysis at 6 to 9 days after transfer. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent. Rosette and total

leaf number on the progeny stem are tightly correlated with the timing of flowering (Koornneef et al (1991) *Mol. Gen. Genet* 229:57-66.

Example I. Full Length Gene Identification and Cloning

For the following examples, G157 refers to SEQ ID Nos 1 and 2, G859 refers to SEQ ID Nos. 3-8, G1842 refers to SEQ ID Nos. 9-16, G1843 refers to SEQ ID Nos. 17 and 18, G1844 refers to SEQ ID Nos. 19-22, G861 refers to SEQ ID Nos. 23-26 and FLC or G1759 refers to SEQ ID Nos. 27, 28.

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

For example, we identified a MADS box gene G157 within BAC F22K20 (GenBank accession AC002291) from Chromosome 1 that was predicted to encode a protein related to FLC. An 872bp cDNA clone for G157 was identified among clones isolated from a library derived from leaf mRNA. The encoded protein was 196 amino acids in length, and shared 62% overall amino acid sequence identity with FLC, and 82% identity within the MADS DNA binding domain.

G157 is also related to G859, G1842, G1843, and G1844 that map together as a tightly linked cluster, at the bottom of chromosome V, that occupies approximately 22 kb and spans three adjacent clones, MXK3, F15O5, and MQN23 (GenBank accession numbers AB019236, AB026633, and AB013395, respectively). G859, G1842, G1843, and G1844 are all arranged in the same orientation. G859, G1842, G1843, and G1844 were likely created by a duplication event; this could have allowed their divergence into different aspects of gene regulation. Their physical proximity suggests that they may act as a unit controlled via common regulatory elements.

The pair-wise comparisons of the 57 amino acid MADS domains of FLC, G157, G859, G1842, G1843, and G1844 are displayed in Table 1. The table shows percent amino acid sequence identity and, in parentheses, the sequence identity percentages when conservative amino acid substitutions are considered. The MADS domains of the proteins encoded by G859, G1842, G1843, and G1844 are highly conserved with those of FLC and G157: these proteins share from 75% to 91% of amino acid sequence identity, depending on the pair-wise comparison as shown below. When conservative amino substitutions are made, the MADS domains of these proteins are 88%-99% identical to each other (shown in parentheses).

Table 1 Percentage of amino acid identity in the MADS domain

	FLC (G1759)	G157	G859	G1842	G1843	G1844
FLC (G1759)	100%	82%(96%)	84%(94%)	77%(91%)	78%(99%)	75%(92%)
G157	-	100%	87%(95%)	89%(94%)	78%(95%)	78%(93%)
G859	-	-	100%	91%(94%)	77%(94%)	78%(92%)
G1842	-	-	-	100%	77%(91%)	78%(88%)
G1843	-	-	-	-	100%	85%(92%)
G1844	-	-	-	-	-	100%

5

Amino acid residue 30 of FLC and by G157, G859, G1842, G1843, and G1844 is an acidic residue (E or D) whereas, in all other *Arabidopsis* MADS domain proteins so far identified, that position is occupied by a positively charged lysine residue. The crystal structure of the human SRF MADS domain bound to DNA has shown that lysine residue (which is also conserved in yeast MCM1 and human MEF2A proteins) to contact the phosphate backbone of the DNA target site (Pellegrini *et al.*, (1995) Nature 376:490-498). That amino acid difference could therefore confer DNA binding properties to FLC and by G157, G859, G1842, G1843, and G1844 distinct from other *Arabidopsis* MADS domain proteins. Therefore, MADS domain proteins with an acidic residue at position 30 may be particularly useful in modifying plant flowering time and vernalization response.

The transcripts from these genes were analyzed by 3' RACE (Rapid Amplification cDNA Ends) and corresponding cDNAs were isolated by RT-PCR from mixed samples of *Arabidopsis* tissue (Columbia ecotype). During this analysis, it was found that G859, G1842 and G1844 transcripts exist in multiple alternatively spliced forms.

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Example II. Flowering Time Associated Genes

Reverse transcriptase PCR was done using gene specific primers within the coding region for each sequence identified. Where possible, the primers were designed near the 3' region of each coding sequence initially identified.

25

Total RNA was isolated from plant tissue and extracted using CTAB. Once extracted total RNA was normalized in concentration across all the tissue types to ensure that the PCR reaction for each tissue received the same amount of cDNA template using the 28S band as reference. Poly A+ was purified using a modified protocol from the Qiagen Oligotex kit batch protocol. cDNA was synthesized using standard protocols. After the first strand cDNA synthesis, primers for Actin 2 were used to normalize the concentration of cDNA across the tissue types. Actin 2 is found to be constitutively expressed in fairly equal levels across the *Arabidopsis* tissue types.

30

For RT PCR, cDNA template was mixed with corresponding primers and Taq polymerase. Each reaction consisted of 0.2 ul cDNA template, 2ul 10X Tricine buffer, and

16.8 ul water, 5pmol Primer 1, 5pmol Primer 2, 0.3 ul Taq polymerase, 200uM dNTPs and 8.6 ul water.

The 96 well plate was covered with microfilm and set in the Thermocycler to start the following reaction cycle. Step1 93° C for 3 mins, Step 2 93° C for 30 sec, Step 3 60-65° C for 1 min, Step 4 72° C for 2 mins,. Steps 2, 3 and 4 were repeated for 20-35 cycles, Step 5 72° C for 5 mins and Step 6 4° C. The PCR plate was sometimes placed back in the thermocycler to amplify more products for 5-15 more cycles to identify genes that have very low expression. The reaction cycle was as follows: Step 2 93° C for 30 sec, Step 3 65° C for 1 min, and Step 4 72° C for 2 ins, repeated for 8 cycles, and Step 4 4° C.

Eight microliters of PCR product and 1.5 ul of loading dye were loaded on a 1.2% agarose gel for analysis between 21 and 36 cycles. Expression levels of specific transcripts were considered low if they were only detectable after 35 cycles of PCR. Expression levels were considered medium or high depending on the levels of transcript compared with observed transcript levels for actin2.

As an example, to assess G157 mRNA levels in G157 plants, PCR was carried out over 25 cycles using primers 5'-GGCATAACCCTTATCGGAGATTGAAGC-3' (SEQ ID No. 57) and 5'-ACACAACTCTGATCTTGTCTCCGAAGG-3' (SEQ ID No. 58). To assess mRNA levels in different tissues extracted from wild type plants, 25 or 30 cycles of PCR were performed using primers 5'-GCATAACCCTTATCGGAGATTGAAGCCAT-3' (SEQ ID No. 59) and 5'-AACATTCTCTCTCATCATCTGTTGCCAGC-3' (SEQ ID No. 60). PCR for *FLC* was performed either with primers 5'-AACGCTTAGTATCTCCGGCGACTTGAAC-3' (SEQ ID No. 51) and 5'-CTCACACGAATAAGGTACAAAGTTCATC-3' (SEQ ID No. 62) over 35 cycles, or 5'-TTAGTATCTCCGGCGACTTGAACCCAAACC-3' (SEQ ID No. 63) and 5'-AGATTCTCAACAAGCTTCAACATGAGTTTCG-3' (SEQ ID No. 64) over 30 cycles. Primer specificity was verified by sequencing RT-PCR products. Samples were standardized via 20-25 cycles of PCR with actin primers.

Example III. Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) *Nucleic Acids Research* 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with Sall and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid

were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l spectinomycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l spectinomycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

Example IV. Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). *Agrobacterium* strain GV3101 was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The integrity of the plasmid construct was verified by PCR amplification and sequence analysis.

Example V. Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l spectinomycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μ M benzylamino purine (Sigma), 200 μ l/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 μ E/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

Example VI. Identification of *Arabidopsis* Primary Transformants

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH

adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination ($50\text{--}75\ \mu\text{E}/\text{m}^2/\text{sec}$) at $22\text{--}23^\circ\text{C}$. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium). Primary transformants are self-crossed and progeny seeds (T_2) collected. T_2 progeny seeds were germinated on kanamycin as described above and kanamycin resistant seedlings were selected, transferred to soil and analyzed.

Example VII. Analysis of transgenic Arabidopsis plants

In a first experiment, G157 plants (ie plants expressing the G157 transgene) were grown in 12 hours light. 31 of 40 lines flowered earlier than control plants transformed with a control vector. Mean rosette leaf number of early T_1 lines was 12.4 ± 0.8 whereas control lines had 27 ± 1.2 rosette leaves. 2 of 40 T_1 plants flowered at the same time as controls and 7 of 40 lines were late flowering and produced visible inflorescences 2 to 3 weeks after wild type.

In further experiments, plants were grown under conditions of 24 hours light at $20\text{--}25^\circ\text{C}$. Under these conditions, the non-transformed control plants produced a mean total of 14.3 ± 0.7 leaves on the primary shoots prior to flower bud initiation. Flower buds were first visible on these plants at a mean of 21.1 ± 0.5 days after sowing (error values represent standard error of the mean to which 95% confidence limits have been attached). For G859, 14/19 T_1 plants were early flowering (mean leaf total of 6.4 ± 0.7 , flower buds visible at 12.9 ± 0.7 days after sowing), 3/19 were wild type, and 2/19 were slightly late flowering compared to wild type (mean total of 19 leaves, flower buds visible at 27 days). RT expression studies revealed that the late flowering individuals possessed the highest levels of transgene expression. These results strongly parallel those obtained for G157. For G1842, 7/10 T_1 flowered early (mean total of 7.9 ± 0.6 leaves, flower buds visible at 13.9 ± 1.0 days), and 3/10 plants were wild type. Overexpression studies were also performed with cDNAs encoding shortened splice variants of G1842. For G1842.2 (encodes a 185 amino acid splice variant), 15/18 T_1 plants flowered early (mean total of 6.9 ± 0.9 leaves, flower buds visible at 14.5 ± 0.6 days) and 3/18 were wild type. For G1842.6 (encodes a 77 amino acid splice variant), 8/10 T_1 plants flowered early mean total of 6.8 ± 1.6 leaves, flower buds visible at 13.9 ± 0.9 days) and 2/10 were wild type. For G1842.7 (encodes a 118 amino acid splice variant) 8/10 T_1 plants flowered early (accurate leaf counts not made) and 2/10 were wild type. Thus, the G1842 splice variants produced comparable effects to the full-length cDNA

clone when over-expressed. For G1843, 7/11 flowered early (mean total of 6.4 ± 0.5 leaves, flower buds visible at 16.0 ± 1.6 days) and 2/11 had a wild type flowering time. The G1843 T1 plants, however, were dwarfed and showed retarded development of some organs. This suggests that G1843 has unpredicted toxic effects when over-expressed. For G1844, 6/10 T1 plants flowered early (mean total of 6.8 ± 1.7 leaves, flower buds visible at 14.7 ± 1.3 days) and 4/10 plants were wild type. Overexpression studies were also performed with a cDNA encoding a shortened splice variant of G1844. For overexpression of G1844.2 (encodes a 184 amino acid splice variant), 6/19 T1 plants flowered early (mean total of 7.8 ± 1.7 leaves, flower buds visible at 15.7 ± 1.3 days) and 13/19 were wild type). The over-expression data for G859, G1842, G1843, and G1844 support the hypothesis that they have a role in the control of flowering time.

RT-PCR was performed on materials from G157 plants using G157 specific primers at approximately 25 cycles. The highest levels of G157 expression were detected in late flowering individual plants or in samples from pooled seedlings that contained late flowering individuals. Plants that showed only moderate or low levels of overexpression compared to wild type were slightly early flowering or normal.

To test whether an increase in G157 could affect flowering time in late flowering ecotypes of Arabidopsis, we overexpressed G157 in the late flowering ecotypes Stockholm and Pitztal. In this experiment, 32 primary transformants from each ecotype were grown interspersed with controls under continuous light conditions. In both ecotypes, around 50% of the transformants flowered earlier than controls, and in some transformants the time to flowering was halved. As was observed with Columbia G157 plants, a minority of Pitztal and Stockholm transformants were clearly later flowering compared to controls.

A correlation between G157 transgene expression and flowering time was also observed in G157 Stockholm and Pitztal T1 plants. RT-PCR was performed with two early and two late flowering lines in each background. Again, the late flowering lines contained the higher levels of G157 expression. Thus, the factor appears to affect flowering time in a quantitative manner; a modest level of overexpression triggers early flowering, whereas a larger increase delays flowering.

In conclusion, over-expression of G157 or any of the related genes modifies flowering time in plants: a modest level of over-expression triggers early flowering, whereas a larger increase delays flowering.

Using similar or identical methodologies described in the examples above, further Arabidopsis genes were identified whose altered expression was correlated with delayed or accelerated flowering. These genes are tabulated in Table 2 with their Sequence Listing Nos., and their effects on flowering time.

Table 2. Further Arabidopsis genes for manipulating flowering time

SEQ ID Nos.	Gene	observations
23, 24	G861	early or late flowering
25, 26	G861.1	early or late flowering
29, 30	G192	late flowering
31, 32	G234	late flowering
33, 34	G361	late flowering
35, 36	G486	late flowering
37, 38	G748	late flowering
39, 40	G994	late flowering
41, 42	G1335	late flowering
43, 44	G562	late flowering
45, 46	G736	late flowering
47, 48	G1073	late flowering
49, 50	G1435	late flowering
51, 52	G180	early flowering
53, 54	G592	early flowering
55, 56	G208	early flowering

5 The vernalization response was also investigated. Late flowering vernalization responsive ecotypes and mutants have high steady state levels of *FLC* transcript, which decrease during the promotion of flowering by vernalization (Michaels and Amasino, (1999) *Plant Cell* 11:949-956; Sheldon et al., (1999) *Plant Cell* 11:445-458; Sheldon et al., (2000) *Proc. Natl. Acad. Sci.* 97: 3735-3758). In contrast to *FLC*, G157 transcript levels show no

10 consistent correlation with the vernalization response in the late flowering Stockholm and Pitztal ecotypes. Additionally we found that over-expression of G157 did not influence *FLC* levels. The effects of vernalization on expression of G861, G859, G1842, G1843, and G1844 were also examined. Germinating seeds of Columbia, Pitztal, Stockholm, *constans-1*, and *fca-9* were vernalized on MS agar plates in a 4°C cold room for 8 weeks, and then transferred

15 to a continuous light growth room. Total tissues from the vernalized seedlings, and freshly sown non-vernalized controls were harvested at 9 days after the transfer. RT-PCR was performed for *FLC*, G157, G859, G1842, G1843, G1844, and G861, and actin. Compared to *FLC* and G157, none of the genes showed a clear consistent decline upon vernalization in the five different sample sets. However, G1844 displayed a converse pattern of expression to

20 *FLC*: G1844 levels consistently increased on vernalization. This is particularly significant as it directly implicates G1844 in control of the vernalization response. Thus G1844 likely activates flowering and has an opposing role to *FLC*.

To explore whether overexpression of G157 produces comparable effects on vernalization, batches of wild type Pitztal and Stockholm seedlings were cold treated for 6 weeks at 4°C, then grown amongst a second selection of G157 T1 Pitztal, G157 T1 Stockholm and non-vernalized wild type plants. As expected, vernalization markedly and uniformly reduced flowering time in both Pitztal and Stockholm wild type plants. Amongst the G157 Stockholm lines, the earliest flowering T1 group (8/23 lines) was indistinguishable from vernalized plants. For Pitztal, however, the early flowering T1 plants were on average marginally later than the vernalized plants. Therefore, overexpression of G157 can substantially reduce the requirement for vernalization in late flowering ecotypes.

Additionally, we observed that the late flowering of G157 lines is independent of FLC expression and does not respond to vernalization. However, the late flowering G157 plants are responsive to photoperiod. In an experiment conducted under short day conditions of 8 hours of light, we obtained a number of G157 Columbia T1 plants that flowered up to a month later than wild type controls (data not shown). To confirm that the late flowering effects caused by G157 overexpression were independent of *FLC* transcription, we tested whether late flowering G157 Columbia plants were responsive to vernalization. No significant change in flowering time was noted: in continuous light conditions, vernalized T2 plants of line 4 had a total of 31.3 +/- 1.8 leaves compared to 30.1 +/- 1.3 when non-vernalized. Control *fca* plants verified that the treatment was effective: vernalized plants flowered after only 10.3 +/- 0.9 leaves compared to more than 40 leaves for the non-vernalized controls. Thus, the late flowering phenotype caused by G157 could not be overcome by vernalization, as would be expected if the delay occurred independently of changes in *FLC* expression.

Example IX. Identification of Homologous Sequences

Homologs from plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919).

The entire NCBI Genbank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI Genbank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs 1-56 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs 1-56, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6e-40 is 3.6×10^{-40} . For up to ten

species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 2.

In addition to P-values, comparisons were also scored by percentage identity.

Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-Arabidopsis genes shown in Figure 2 and the Arabidopsis genes in the sequence listing are: SEQ ID No. 1: 54%-67%; SEQ ID Nos. 3,5,7: 37%-47%; SEQ ID Nos. 9,11,13,15: 54%-62%; SEQ ID No. 17: 62%-71%; SEQ ID Nos. 19, 21: 50%-67%; SEQ ID Nos. 23,25: 75%-91%; SEQ ID No. 27: 46%-69%; SEQ ID No. 29: 44%-90%; SEQ ID No. 31: 57-89%; SEQ ID No. 33: 37%-79%; SEQ ID No. 35: 50%-71%; SEQ ID No. 37: 39%-63%; SEQ ID No. 39: 58%-70%; SEQ ID No. 41: 45%-73%; SEQ ID No. 43: 42%-84%; SEQ ID No. 45: 47%-81%; SEQ ID No. 47: 31%-71%; SEQ ID No. 49: 40%-67%; SEQ ID No. 51: 69%-51%; SEQ ID No. 53: 43%-86%; and SEQ ID No. 55: 79%-89%.

Arabidopsis homologs of genes in Table 2 were also identified using BLAST. These genes are found in the following Arabidopsis BAC sequences, identified by their Genbank sequence NID numbers: 2827698 (G234 homolog), 3241917 (G748 homolog), 2618604 (G994 homolog), 6598548 (G1335 homolog), 7340331 (G736 homolog), 6523051 (G1435 homolog), 6598491 (G208 homolog) and 3172156 (G208 homolog).

All references (publications and patents) are incorporated herein by reference in their entirety for all purposes.

Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

Figure 1

SEQ ID No.	Gene	cDNA or	conserved domain
1	G157	cDNA	
2	G157	protein	2-57
3	G859	cDNA	
4	G859	protein	2-57
5	G859.1	cDNA	
6	G859.1	protein	2-57
7	G859.2	cDNA	
8	G859.2	protein	2-57
9	G1842	cDNA	
10	G1842	protein	2-57
11	G1842.2	cDNA	
12	G1842.2	protein	2-57
13	G1842.6	cDNA	
14	G1842.6	protein	2-57
15	G1842.7	cDNA	
16	G1842.7	protein	2-57
17	G1843	cDNA	
18	G1843	protein	2-57
19	G1844	cDNA	
20	G1844	protein	2-57
21	G1844.2	cDNA	
22	G1844.2	protein	2-57
23	G861	cDNA	
24	G861	protein	2-57
25	G861.1	cDNA	
26	G861.1	protein	2-57
27	G1759	cDNA	
28	G1759	protein	2-57
29	G192	cDNA	
30	G192	protein	128-185
31	G234	cDNA	
32	G234	protein	14-115
33	G361	cDNA	
34	G361	protein	43-63
35	G486	cDNA	
36	G486	protein	5-66
37	G748	cDNA	
38	G748	protein	112-140
39	G994	cDNA	
40	G994	protein	14-123
41	G1335	cDNA	
42	G1335	protein	24-43, 131-144, 185-203
43	G562	cDNA	
44	G562	protein	253-315
45	G736	cDNA	
46	G736	protein	54-111
47	G1073	cDNA	
48	G1073	protein	33-42, 78-175
49	G1435	cDNA	
50	G1435	protein	146-194
51	G180	cDNA	
52	G180	protein	118-174
53	G592	cDNA	
54	G592	protein	290-342
55	G208	cDNA	
56	G208	protein	14-116

Figure 2A

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
1	G157	6530836	3.10E-22	Lycopersicon esculentum
1	G157	5606765	5.50E-14	Glycine max
1	G157	6826955	1.20E-13	Zea mays
1	G157	6536942	6.00E-13	Medicago truncatula
1	G157	8707754	1.40E-12	Hordeum vulgare
1	G157	2293891	1.40E-12	Petunia x hybrida
1	G157	19870	1.40E-12	Nicotiana tabacum
1	G157	7628118	3.70E-12	Gossypium arboreum
1	G157	5050220	3.80E-12	Gossypium hirsutum
1	G157	9414215	4.50E-12	Triticum aestivum
3,5,7	G859	6530836	1.40E-34	Lycopersicon esculentum
3,5,7	G859	5777903	4.70E-30	Malus domestica
3,5,7	G859	9367312	7.10E-30	Hordeum vulgare
3,5,7	G859	6467973	3.60E-29	Dendrobium grex Madame Thong-IN
3,5,7	G859	4204233	1.20E-28	Lolium temulentum
3,5,7	G859	939784	2.50E-28	Zea mays
3,5,7	G859	6651032	3.10E-28	Capsicum annuum
3,5,7	G859	1483227	4.60E-28	Betula pendula
3,5,7	G859	5295983	8.70E-28	Oryza sativa
3,5,7	G859	5070137	1.10E-27	Nicotiana sylvestris
9,11,13,15	G1842	6530836	5.90E-19	Lycopersicon esculentum
9,11,13,15	G1842	5606765	8.00E-15	Glycine max
9,11,13,15	G1842	6826955	1.20E-12	Zea mays
9,11,13,15	G1842	4979250	1.50E-11	Oryza sativa
9,11,13,15	G1842	6536942	1.50E-11	Medicago truncatula
9,11,13,15	G1842	7501504	4.00E-11	Gossypium arboreum
9,11,13,15	G1842	9444818	4.70E-11	Triticum aestivum
9,11,13,15	G1842	5859176	5.40E-11	Pinus taeda
9,11,13,15	G1842	5777905	6.80E-11	Malus domestica
9,11,13,15	G1842	6647105	6.80E-11	Mesembryanthemum crystallinum
17	G1843	8707754	6.60E-15	Hordeum vulgare
17	G1843	5606765	1.10E-14	Glycine max
17	G1843	4387730	1.50E-14	Lycopersicon esculentum
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19, 21	G1844	9429009	4.40E-13	Triticum aestivum
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19, 21	G1844	6530836	1.40E-12	Lycopersicon esculentum
19, 21	G1844	6918768	1.70E-12	Zea mays
19, 21	G1844	6536942	3.50E-12	Medicago truncatula
19, 21	G1844	2252481	3.70E-12	Ceratopteris richardii
23,25	G861	5601313	8.20E-49	Lycopersicon esculentum
23,25	G861	2735763	1.50E-37	Solanum tuberosum
23,25	G861	6652755	5.40E-37	Paulownia kawakamii

Figure 2B

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
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23,25	G861	3986688	5.20E-26	Cichorium intybus
23,25	G861	7552197	2.40E-25	Sorghum bicolor
23,25	G861	5295977	4.90E-24	Oryza sativa
23,25	G861	9194959	3.60E-19	Medicago truncatula
23,25	G861	3855425	4.40E-19	Populus tremula x Populus tremuloides
27	G1759	5606765	4.60E-16	Glycine max
27	G1759	7647685	4.10E-15	Lycopersicon esculentum
27	G1759	4979250	2.70E-14	Oryza sativa
27	G1759	8707754	6.30E-14	Hordeum vulgare
27	G1759	5777905	6.80E-14	Malus domestica
27	G1759	7626240	1.10E-13	Gossypium arboreum
27	G1759	5047371	1.10E-13	Gossypium hirsutum
27	G1759	6918768	1.20E-13	Zea mays
27	G1759	8574456	1.30E-13	Capsicum annuum
27	G1759	8216956	1.30E-13	Cucumis sativus
29	G192	7284340	3.60E-40	Glycine max
29	G192	7779802	1.10E-39	Lotus japonicus
29	G192	9361307	9.40E-28	Triticum aestivum
29	G192	7340336	8.10E-24	Oryza sativa
29	G192	6529152	4.70E-23	Lycopersicon esculentum
29	G192	7206269	2.90E-22	Medicago truncatula
29	G192	4886128	4.50E-15	Zea mays
29	G192	8706346	4.70E-13	Hordeum vulgare
29	G192	9302479	8.80E-13	Sorghum bicolor
29	G192	3326241	2.40E-12	Gossypium hirsutum
31	G234	9193243	7.50E-60	Medicago truncatula
31	G234	9264511	3.30E-57	Glycine max
31	G234	7412424	3.60E-49	Lycopersicon esculentum
31	G234	8335078	2.60E-48	Oryza sativa
31	G234	7218651	1.00E-42	Sorghum bicolor
31	G234	9364630	9.90E-40	Triticum aestivum
31	G234	6079814	5.10E-36	Gossypium arboreum
31	G234	9252441	5.40E-35	Solanum tuberosum
31	G234	5860031	1.00E-33	Pinus taeda
31	G234	5050757	2.60E-33	Gossypium hirsutum
33	G361	7561045	2.30E-21	Medicago truncatula
33	G361	9307604	1.20E-17	Sorghum bicolor
33	G361	4119050	1.70E-13	Oryza sativa
33	G361	8175037	7.30E-13	Hordeum vulgare
33	G361	8329902	5.30E-09	Mesembryanthemum crystallinum
33	G361	6534259	1.20E-08	Lycopersicon esculentum
33	G361	7283798	1.30E-08	Glycine max
33	G361	3854369	5.50E-08	Populus tremula x Populus tremuloides
33	G361	9365078	1.70E-07	Triticum aestivum
33	G361	5268965	0.00023	Zea mays
35	G486	6845875	3.10E-36	Glycine max
35	G486	8172030	4.20E-29	Medicago truncatula
35	G486	9416562	6.40E-29	Triticum aestivum
35	G486	5050127	4.90E-28	Gossypium hirsutum
35	G486	7628400	6.10E-28	Gossypium arboreum
35	G486	7781090	2.10E-27	Lotus japonicus

Figure 2C

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
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35	G486	7409616	1.30E-26	Lycopersicon esculentum
35	G486	8071558	1.40E-26	Solanum tuberosum
37	G748	853689	5.60E-87	Cucurbita maxima
37	G748	7242897	3.10E-59	Oryza sativa
37	G748	5888560	9.70E-46	Lycopersicon esculentum
37	G748	6341666	4.50E-38	Glycine max
37	G748	9190140	2.90E-35	Medicago truncatula
37	G748	7535776	4.00E-33	Sorghum bicolor
37	G748	9419494	1.70E-31	Hordeum vulgare
37	G748	9410157	8.20E-29	Triticum aestivum
37	G748	3929324	3.50E-25	Dendrobium grex Madame Thong-IN
37	G748	6020953	7.30E-21	Zea mays
39	G994	6651291	1.50E-55	Pimpinella brachycarpa
39	G994	7561750	5.60E-51	Medicago truncatula
39	G994	5268844	2.10E-50	Zea mays
39	G994	1430845	3.10E-50	Lycopersicon esculentum
39	G994	1945282	5.40E-49	Oryza sativa
39	G994	22637	1.40E-46	Physcomitrella patens
39	G994	7626566	4.40E-44	Gossypium arboreum
39	G994	2921339	4.50E-44	Gossypium hirsutum
39	G994	7590249	3.60E-43	Glycine max
39	G994	20562	6.30E-43	Petunia x hybrida
41	G1335	19742	8.40E-63	Nicotiana glauca
41	G1335	5398738	1.20E-59	Zea mays
41	G1335	9361467	1.40E-50	Triticum aestivum
41	G1335	8330366	1.60E-48	Mesembryanthemum crystallinum
41	G1335	8174823	7.50E-43	Hordeum vulgare
41	G1335	6696628	8.00E-42	Pinus taeda
41	G1335	7721100	1.20E-39	Lotus japonicus
41	G1335	7502173	2.60E-37	Gossypium arboreum
41	G1335	1817176	5.60E-36	Pinus radiata
41	G1335	7550978	3.30E-35	Sorghum bicolor
43	G562	1399004	6.60E-142	Brassica napus
43	G562	5381310	6.80E-53	Catharanthus roseus
43	G562	169958	3.80E-45	Glycine max
43	G562	2879779	3.60E-43	Spinacia oleracea
43	G562	7565950	2.10E-41	Medicago truncatula
43	G562	728627	4.50E-41	Nicotiana tabacum
43	G562	1155053	2.30E-40	Phaseolus vulgaris
43	G562	1498300	5.70E-40	Petroselinum crispum
43	G562	5046889	6.70E-34	Gossypium hirsutum
43	G562	8328888	2.60E-25	Mesembryanthemum crystallinum
45	G736	7409627	1.40E-37	Lycopersicon esculentum
45	G736	9197391	5.60E-32	Medicago truncatula
45	G736	9419494	4.70E-27	Hordeum vulgare
45	G736	7328718	1.30E-25	Oryza sativa
45	G736	9410157	1.80E-25	Triticum aestivum
45	G736	853689	5.20E-25	Cucurbita maxima
45	G736	7535776	6.60E-25	Sorghum bicolor
45	G736	3929324	4.70E-21	Dendrobium grex Madame Thong-IN
45	G736	2393774	9.60E-20	Zea mays

Figure 2D

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
45	G736	7624398	1.10E-19	Gossypium arboreum
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47	G1073	6846994	2.50E-44	Glycine max
47	G1073	7615218	1.60E-42	Lotus japonicus
47	G1073	7333102	2.70E-34	Lycopersicon esculentum
47	G1073	9445090	3.40E-25	Triticum aestivum
47	G1073	9252370	2.20E-24	Solanum tuberosum
47	G1073	5042437	4.60E-21	Oryza sativa
47	G1073	7536402	5.30E-20	Sorghum bicolor
47	G1073	2213535	7.30E-19	Pisum sativum
47	G1073	7624850	2.10E-18	Gossypium arboreum
49	G1435	9203811	3.70E-37	Glycine max
49	G1435	9430136	4.10E-35	Lycopersicon esculentum
49	G1435	8904354	4.30E-32	Hordeum vulgare
49	G1435	5050706	3.30E-26	Gossypium hirsutum
49	G1435	7614196	6.40E-19	Lotus japonicus
49	G1435	7551484	1.00E-18	Sorghum bicolor
49	G1435	6916552	7.20E-12	Lycopersicon pennellii
49	G1435	2443007	5.50E-11	Oryza sativa
49	G1435	9255229	1.30E-10	Zea mays
49	G1435	7766737	2.80E-10	Medicago truncatula
51	G180	8468047	1.90E-35	Oryza sativa
51	G180	7559831	1.20E-24	Medicago truncatula
51	G180	5272716	9.90E-24	Lycopersicon esculentum
51	G180	9187621	3.30E-23	Solanum tuberosum
51	G180	6566312	1.30E-22	Glycine max
51	G180	9304207	1.30E-21	Sorghum bicolor
51	G180	7721184	1.30E-20	Lotus japonicus
51	G180	9444636	3.10E-19	Triticum aestivum
51	G180	3220212	5.20E-19	Gossypium hirsutum
51	G180	1159876	8.00E-19	Avena fatua
53	G592	7924069	7.10E-27	Glycine max
53	G592	5896650	1.10E-22	Lycopersicon esculentum
53	G592	6279773	1.10E-17	Lycopersicon pennellii
53	G592	9364330	1.20E-14	Triticum aestivum
53	G592	6166282	5.40E-14	Pinus taeda
53	G592	8367093	1.60E-12	Zea mays
53	G592	9301543	6.60E-11	Sorghum bicolor
53	G592	7562632	2.80E-10	Medicago truncatula
53	G592	702652	5.80E-05	Oryza sativa
53	G592	7322923	0.094	Lycopersicon hirsutum
55	G208	437326	2.80E-65	Gossypium hirsutum
55	G208	7765706	4.40E-64	Medicago truncatula
55	G208	5269878	5.80E-64	Lycopersicon esculentum
55	G208	19054	6.90E-63	Hordeum vulgare
55	G208	2605616	1.00E-62	Oryza sativa
55	G208	7626566	3.50E-62	Gossypium arboreum
55	G208	6667606	4.10E-62	Glycine max
55	G208	517492	1.80E-60	Zea mays
55	G208	9302672	2.40E-57	Sorghum bicolor
55	G208	5860031	1.30E-54	Pinus taeda

We Claim:

1. A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28 but excluding SEQ ID No. 28, wherein said transgenic plant has (i) a modified flowering time compared with another plant lacking the recombinant polynucleotide or (ii) a modified vernalization requirement compared with another plant lacking the recombinant polynucleotide.

2. The transgenic plant of claim 1, wherein the nucleotide sequence encodes a polypeptide comprising a conserved domain selected from the group consisting of conserved domains of SEQ ID Nos. 2N, where N=1-28.

3. The transgenic plant of claim 1, wherein the recombinant polynucleotide further comprises a promoter operably linked to said nucleotide sequence.

4. The transgenic plant of claim 3, wherein said promoter is constitutive or inducible or tissue-active.

5. The transgenic plant of claim 1, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28.

6. A method for altering the flowering time or vernalization requirement of a plant, said method comprising (a) transforming a plant with a recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising at least 6 consecutive amino acids of a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28 but excluding SEQ ID No. 28, (b) selecting said transformed plants; and (c) identifying a transformed plant having an altered flowering time.

7. The method of claim 6, wherein the nucleotide sequence encodes a polypeptide comprising a conserved domain selected from the group consisting of conserved domains of SEQ ID Nos. 2N, where N=1-28.

8. The method of claim 6, wherein the recombinant polynucleotide further comprises a promoter operably linked to said nucleotide sequence.

9. The method of claim 8, wherein said promoter is constitutive or inducible or tissue-active.

10. The method of claim 1, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28.

11. A method for altering the flowering time or vernalization requirement of a plant, said method comprising (a) transforming the plant with a recombinant polynucleotide comprising a nucleotide sequence comprising at least 18 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2N-1, where N= 1-28, but excluding SEQ ID No. 27; and (b) selecting said transformed plant.

12. The method of claim 11, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28.

13. A method for altering a plant's flowering time or vernalization requirement, said method comprising (a) providing a database sequence; (b) comparing said database sequence with a polypeptide selected from SEQ ID Nos. 2N, where N= 1-28; (c) selecting a database sequence that meets selected sequence criteria; and (d) transforming said selected database sequence in the plant.

14. The method of claim 13, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28.

15. A method for altering a plant's flowering time or vernalization requirement, said method comprising (a) providing a database sequence; (b) comparing said database sequence with a polynucleotide selected from SEQ ID Nos. 2N-1, where N= 1-28; (c) selecting a database sequence that meets selected sequence criteria; and (d) transforming said selected database sequence in the plant.

16. The method of claim 15, wherein said recombinant polynucleotide encodes a polypeptide comprising a conserved domain having greater than an 84% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2N, where N=1-28.

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cagaaaaaat	tcggaattat	cttccacaca	aggagttact	agaaatagtc	caaagattct											789
ctaatatcta	tggaggaaca	gctcgagact	gctctgtcag	taattagagc	taagaagaca											849
gaactaatga	tggaggatat	gaagtcactt	caagaaaggg	agaagttgct	gatagaagag											909
aaccagattc	tggctagcca	ggtggggaag	aagacgtttc	tggttataga	aggtgacaga											969
ggaatgtcat	gggaaaatgg	ctccggcaac	aaagtacggg	agactcttcc	gctgctcaag											1029
taatcaccat	catcaacggc	tgagctttca	ccttaaaactt	acagcctgat	tcagaagttt											1089
ttacaaaattt	gtaaattata	aaaagcttca	taataatctc	aaccttttta	tcttctctgc											1149
gccaatgtgg	aaattaaggt	aaaccaaaaa	aaaaaaaaaa	aaaaaaa												1196

<210> 4
 <211> 145
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 4

MBI-0021.txt

Met Gly Arg Lys Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Leu Val Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Lys Ser Ala Ser Gly Asp Asn Met Ser
 50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu Leu Glu Ala
 65 70 75 80

Leu Asp Leu Ala Glu Lys Thr Arg Asn Tyr Leu Pro Leu Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Arg Leu Ala Gln Arg His Phe Tyr Leu Pro Leu
 100 105 110

Leu Leu Met Lys Asn Thr Phe Phe Phe Leu Phe Phe Trp Arg Ile Met
 115 120 125

Asn Thr Ala Ser Leu Lys Asn Gln Met Ser Ile Met Gln Val Trp Ile
 130 135 140

Leu
 145

<210> 5
 <211> 972
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (132)..(569)
 <223> G859.1

<400> 5
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agcaaaaaaac attgtgggtc tccggtgatt aggatcaaatt tagggcacca gccttatcgg 120

aggaagaagc c atg ggt aga aaa aaa gtc gag atc aag cga atc gag aac 170
 Met Gly Arg Lys Lys Val Glu Ile Lys Arg Ile Glu Asn
 1 5 10

aaa agt agt cga caa gtc act ttc tcc aaa cga cgc aat ggt ctc atc 218
 Lys Ser Ser Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile
 15 20 25

MBI-0021.txt

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gag aaa gct cga caa ctt tca att ctc tgt gaa tct tcc atc gct gtt      266
Glu Lys Ala Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val
30                      35                      40                      45

ctc gtc gtc tcc ggc tcc gga aaa ctc tac aag tct gcc tcc ggt gac      314
Leu Val Val Ser Gly Ser Gly Lys Leu Tyr Lys Ser Ala Ser Gly Asp
                      50                      55                      60

aac atg tca aag atc att gat cgt tac gaa ata cat cat gct gat gaa      362
Asn Met Ser Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu
                      65                      70                      75

ctt gaa gcc tta gat ctt gca gaa aaa act cgg aat tat ctg cca ctc      410
Leu Glu Ala Leu Asp Leu Ala Glu Lys Thr Arg Asn Tyr Leu Pro Leu
                      80                      85                      90

aaa gag tta cta gaa ata gtc caa agg tta gca caa aga cac ttt tat      458
Lys Glu Leu Leu Glu Ile Val Gln Arg Leu Ala Gln Arg His Phe Tyr
                      95                      100                      105

ctc cct ctt ctt ctg atg aaa aat act ttt ttt ttt ctt ttc ttt tgg      506
Leu Pro Leu Leu Leu Met Lys Asn Thr Phe Phe Phe Leu Phe Phe Trp
110                      115                      120                      125

cga att atg aat aca gca agc ttg aag aat caa atg tcg ata atg caa      554
Arg Ile Met Asn Thr Ala Ser Leu Lys Asn Gln Met Ser Ile Met Gln
                      130                      135                      140

gtg tgg ata ctt taa tttctctgga ggaacagctc gagactgctc tgtccgtaac      609
Val Trp Ile Leu
                      145

tagagctagg aagacagaac taatgatggg ggaagtgaag tcccttcaaa aaacggagaa      669

cttgctgaga gaagagaacc agactttggc tagccaggtg gggaagaaga cgtttctggt      729

tatagaaggt gacagaggaa tgtcatggga aaatggctcc ggcaacaaaag tacgggagac      789

tcttcgctg ctcaagtaat caccatcatc aacggctgag ctttcacctt aaacttacag      849

cctgattcag aagtttttac aaatttgtaa attataaaaa gcttcataat aatctcaacc      909

tttttatctt cctcgcgcca atgtggaaat taaggtaaac caaaaaaaaaa aaaaaaaaaa      969

aaa                                                                972

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<210> 6
 <211> 145
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6

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Met Gly Arg Lys Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1                      5                      10                      15

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Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
20                      25                      30

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MBI-0021.txt

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Leu Val Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Lys Ser Ala Ser Gly Asp Asn Met Ser
 50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu Leu Glu Ala
 65 70 75 80

Leu Asp Leu Ala Glu Lys Thr Arg Asn Tyr Leu Pro Leu Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Arg Leu Ala Gln Arg His Phe Tyr Leu Pro Leu
 100 105 110

Leu Leu Met Lys Asn Thr Phe Phe Phe Leu Phe Phe Trp Arg Ile Met
 115 120 125

Asn Thr Ala Ser Leu Lys Asn Gln Met Ser Ile Met Gln Val Trp Ile
 130 135 140

Leu
 145

<210> 7
 <211> 1036
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (162)..(752)
 <223> G859.2

<400> 7
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 gagagagaga gaaacgaaga aaaaaaaga agcaaaaaac attgtgggtc tccggtgatt 120
 aggatcaaat tagggcacca gccttatcgg aggaagaagc c atg ggt aga aaa aaa 176
 Met Gly Arg Lys Lys
 1 5

gtc gag atc aag cga atc gag aac aaa agt agt cga caa gtc act ttc 224
 Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg Gln Val Thr Phe
 10 15 20

tcc aaa cga cgc aat ggt ctc atc gag aaa gct cga caa ctt tca att 272
 Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala Arg Gln Leu Ser Ile
 25 30 35

ctc tgt gaa tct tcc atc gct gtt ctc gtc gtc tcc ggc tcc gga aaa 320
 Leu Cys Glu Ser Ser Ile Ala Val Leu Val Val Ser Gly Ser Gly Lys
 40 45 50

MBI-0021.txt

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ctc tac aag tct gcc tcc ggt gac aac atg tca aag atc att gat cgt      368
Leu Tyr Lys Ser Ala Ser Gly Asp Asn Met Ser Lys Ile Ile Asp Arg
   55                                60                                65

tac gaa ata cat cat gct gat gaa ctt gaa gcc tta gat ctt gca gaa      416
Tyr Glu Ile His His Ala Asp Glu Leu Glu Ala Leu Asp Leu Ala Glu
   70                                75                                80                                85

aaa act cgg aat tat ctg cca ctc aaa gag tta cta gaa ata gtc caa      464
Lys Thr Arg Asn Tyr Leu Pro Leu Lys Glu Leu Leu Glu Ile Val Gln
   90                                95                                100

agc aag ctt gaa gaa tca aat gtc gat aat gca agt gtg gat act tta      512
Ser Lys Leu Glu Glu Ser Asn Val Asp Asn Ala Ser Val Asp Thr Leu
  105                                110                                115

att tct ctg gag gaa cag ctc gag act gct ctg tcc gta act aga gct      560
Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Thr Arg Ala
  120                                125                                130

agg aag aca gaa cta atg atg ggg gaa gtg aag tcc ctt caa aaa acg      608
Arg Lys Thr Glu Leu Met Met Gly Glu Val Lys Ser Leu Gln Lys Thr
  135                                140                                145

gag aac ttg ctg aga gaa gag aac cag act ttg gct agc cag gtg ggg      656
Glu Asn Leu Leu Arg Glu Glu Asn Gln Thr Leu Ala Ser Gln Val Gly
  150                                155                                160                                165

aag aag acg ttt ctg gtt ata gaa ggt gac aga gga atg tca tgg gaa      704
Lys Lys Thr Phe Leu Val Ile Glu Gly Asp Arg Gly Met Ser Trp Glu
  170                                175                                180

aat ggc tcc ggc aac aaa gta cgg gag act ctt ccg ctg ctc aag taa      752
Asn Gly Ser Gly Asn Lys Val Arg Glu Thr Leu Pro Leu Leu Lys
  185                                190                                195

tcaccatcat caacggctga gctttcacct taaacttaca gcctgattca gaagttttta      812

caaatttgta aattataaaa agcttcataa taatctcaac ctttttatct tcctcgcgcc      872

aatgtggaaa ttaagggttaa aaataaaata aaacagaagc tcatgcgaaa gaattgtaaa      932

actaagataa agctatagta gatctttatt gtaccttcgt agacgatata agattttattc      992

gtgtgtttgt cttcccctcn aaaaaaaaaa aaaaaaaaaa aaaa                    1036

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<210> 8
<211> 196
<212> PRT
<213> Arabidopsis thaliana

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<400> 8

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Met Gly Arg Lys Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1          5          10          15

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Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
20          25          30

```

MBI-0021.txt

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Leu Val Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Lys Ser Ala Ser Gly Asp Asn Met Ser
 50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu Leu Glu Ala
 65 70 75 80

Leu Asp Leu Ala Glu Lys Thr Arg Asn Tyr Leu Pro Leu Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Ser Lys Leu Glu Glu Ser Asn Val Asp Asn Ala
 100 105 110

Ser Val Asp Thr Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu
 115 120 125

Ser Val Thr Arg Ala Arg Lys Thr Glu Leu Met Met Gly Glu Val Lys
 130 135 140

Ser Leu Gln Lys Thr Glu Asn Leu Leu Arg Glu Glu Asn Gln Thr Leu
 145 150 155 160

Ala Ser Gln Val Gly Lys Lys Thr Phe Leu Val Ile Glu Gly Asp Arg
 165 170 175

Gly Met Ser Trp Glu Asn Gly Ser Gly Asn Lys Val Arg Glu Thr Leu
 180 185 190

Pro Leu Leu Lys
 195

<210> 9
 <211> 1059
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (219)..(809)
 <223> G1842

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 tctctatcgt ctaacaaaaa aaaaaactga cttgggattt tttttcattt gtctagccca 120
 aaagaagaag atagaaacga agaaaaaaag caaacacatt ttgggtcccc ggtggttagg 180
 atcaaattag ggcacaaacc ttatcggaaga aagaagcc atg gga aga aga aaa gtc 236

MBI-0021.txt

Met Gly Arg Arg Lys Val
1 5

gag atc aag cga atc gag aac aaa agc agt cga caa gtc act ttc tcc	284
Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg Gln Val Thr Phe Ser	
10 15 20	
aaa cga cgc aaa ggt ctc atc gaa aaa gct cga caa ctt tca att ctc	332
Lys Arg Arg Lys Gly Leu Ile Glu Lys Ala Arg Gln Leu Ser Ile Leu	
25 30 35	
tgt gaa tct tcc atc gct gtt gtc gcc gtc tcc ggt tcc gga aaa ctc	380
Cys Glu Ser Ser Ile Ala Val Val Ala Val Ser Gly Ser Gly Lys Leu	
40 45 50	
tac gac tct gcc tcc ggt gac aac atg tca aag atc att gat cgt tat	428
Tyr Asp Ser Ala Ser Gly Asp Asn Met Ser Lys Ile Ile Asp Arg Tyr	
55 60 65 70	
gaa ata cat cat gct gat gaa ctt aaa gcc tta gat ctt gca gaa aaa	476
Glu Ile His His Ala Asp Glu Leu Lys Ala Leu Asp Leu Ala Glu Lys	
75 80 85	
att cgg aat tat ctt cca cac aag gag tta cta gaa ata gtc caa agc	524
Ile Arg Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Ile Val Gln Ser	
90 95 100	
aag ctt gaa gaa tca aat gtc gat aat gta agt gta gat tct cta ata	572
Lys Leu Glu Glu Ser Asn Val Asp Asn Val Ser Val Asp Ser Leu Ile	
105 110 115	
tct atg gag gaa cag ctc gag act gct ctg tca gta att aga gct aag	620
Ser Met Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ile Arg Ala Lys	
120 125 130	
aag aca gaa cta atg atg gag gat atg aag tca ctt caa gaa agg gag	668
Lys Thr Glu Leu Met Glu Asp Met Lys Ser Leu Gln Glu Arg Glu	
135 140 145 150	
aag ttg ctg ata gaa gag aac cag att ctg gct agc cag gtg ggg aag	716
Lys Leu Leu Ile Glu Glu Asn Gln Ile Leu Ala Ser Gln Val Gly Lys	
155 160 165	
aag acg ttt ctg gtt ata gaa ggt gac aga gga atg tca cgg gaa aat	764
Lys Thr Phe Leu Val Ile Glu Gly Asp Arg Gly Met Ser Arg Glu Asn	
170 175 180	
ggc tcc ggc aac aaa gta ccg gag act ctt tcg ctg ctc aag taa	809
Gly Ser Gly Asn Lys Val Pro Glu Thr Leu Ser Leu Leu Lys	
185 190 195	
tcaccatcat caacggctga gctttcacca taaacttact cacagcctga ttcagaagct	869
tttacaaaat tgtaaattat aaaaagctgc ataataatct caaccttttt atcttcctcg	929
cgccaatgtg gaaataaagg taaaacaaaa cgaagctctt ttcttttatg cgaaagaatt	989
gtaaaactaa gataaagcta ccgatctttg ttgtacctta gtagacaaat atcagagttc	1049
ttgtgcttgt	1059

<210> 10

MBI-0021.txt

<211> 196

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15 20

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Val Ala Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Asp Ser Ala Ser Gly Asp Asn Met Ser
 50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu Leu Lys Ala
 65 70 75 80

Leu Asp Leu Ala Glu Lys Ile Arg Asn Tyr Leu Pro His Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Ser Lys Leu Glu Glu Ser Asn Val Asp Asn Val
 100 105 110

Ser Val Asp Ser Leu Ile Ser Met Glu Glu Gln Leu Glu Thr Ala Leu
 115 120 125

Ser Val Ile Arg Ala Lys Lys Thr Glu Leu Met Met Glu Asp Met Lys
 130 135 140

Ser Leu Gln Glu Arg Glu Lys Leu Leu Ile Glu Glu Asn Gln Ile Leu
 145 150 155 160

Ala Ser Gln Val Gly Lys Lys Thr Phe Leu Val Ile Glu Gly Asp Arg
 165 170 175

Gly Met Ser Arg Glu Asn Gly Ser Gly Asn Lys Val Pro Glu Thr Leu
 180 185 190

Ser Leu Leu Lys
 195

<210> 11

<211> 880

<212> DNA

<213> Arabidopsis thaliana

MBI-0021.txt

<220>

<221> CDS

<222> (79) .. (636)

<223> G1842.2

<400> 11

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ttatcgggaga aagaagcc  atg gga aga aga aaa gtc gag atc aag cga atc      111
                      Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile
                      1          5          10

gag aac aaa agc agt cga caa gtc act ttc tcc aaa cga cgc aaa ggt      159
Glu Asn Lys Ser Ser Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly
                      15          20          25

ctc atc gaa aaa gct cga caa ctt tca att ctc tgt gaa tct tcc atc      207
Leu Ile Glu Lys Ala Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile
                      30          35          40

gct gtt gtc gcc gtc tcc ggt tcc gga aaa ctc tac gac tct gcc tcc      255
Ala Val Val Ala Val Ser Gly Ser Gly Lys Leu Tyr Asp Ser Ala Ser
                      45          50          55

ggt gac aac atg tca aag atc att gat cgt tat gaa ata cat cat gct      303
Gly Asp Asn Met Ser Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala
60          65          70          75

gat gaa ctt aaa gcc tta gat ctt gca gaa aaa att cgg aat tat ctt      351
Asp Glu Leu Lys Ala Leu Asp Leu Ala Glu Lys Ile Arg Asn Tyr Leu
                      80          85          90

cca cac aag gag tta cta gaa ata gtc caa agt gta gat tct cta ata      399
Pro His Lys Glu Leu Leu Glu Ile Val Gln Ser Val Asp Ser Leu Ile
                      95          100          105

tct atg gag gaa cag ctc gag act gct ctg tca gta att aga gct aag      447
Ser Met Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ile Arg Ala Lys
110          115          120

aag aca gaa cta atg atg gag gat atg aag tca ctt caa gaa agg gag      495
Lys Thr Glu Leu Met Met Glu Asp Met Lys Ser Leu Gln Glu Arg Glu
125          130          135

aag ttg ctg ata gaa gag aac cag att ctg gct agc cag gtg ggg aag      543
Lys Leu Leu Ile Glu Glu Asn Gln Ile Leu Ala Ser Gln Val Gly Lys
140          145          150          155

aag acg ttt ctg gtt ata gaa ggt gac aga gga atg tca cgg gaa aat      591
Lys Thr Phe Leu Val Ile Glu Gly Asp Arg Gly Met Ser Arg Glu Asn
160          165          170

ggc tcc ggc aac aaa gta ccg gag act ctt tcg ctg ctc aag taa      636
Gly Ser Gly Asn Lys Val Pro Glu Thr Leu Ser Leu Leu Lys
175          180          185

tcaccatcat caacggctga gctttcacca taaacttact cacagcctga ttcagaagct      696

tttacaaaat tgtaaattat aaaaagctgc ataataatct caaccttttt atcttcctcg      756

cgccaatgtg gaaataaagg taaaacaaaa cgaagctctt ttcttttatg cgaaagaatt      816

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MBI-0021.txt

gtaaaactaa gataaagcta ccgatctttg ttgtacctta gtagacaaat atcagagttc 876
 ttgt 880

<210> 12
 <211> 185
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 12

Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Val Ala Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Asp Ser Ala Ser Gly Asp Asn Met Ser
 50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu Leu Lys Ala
 65 70 75 80

Leu Asp Leu Ala Glu Lys Ile Arg Asn Tyr Leu Pro His Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Ser Val Asp Ser Leu Ile Ser Met Glu Glu Gln
 100 105 110

Leu Glu Thr Ala Leu Ser Val Ile Arg Ala Lys Lys Thr Glu Leu Met
 115 120 125

Met Glu Asp Met Lys Ser Leu Gln Glu Arg Glu Lys Leu Leu Ile Glu
 130 135 140

Glu Asn Gln Ile Leu Ala Ser Gln Val Gly Lys Lys Thr Phe Leu Val
 145 150 155 160

Ile Glu Gly Asp Arg Gly Met Ser Arg Glu Asn Gly Ser Gly Asn Lys
 165 170 175

Val Pro Glu Thr Leu Ser Leu Leu Lys
 180 185

<210> 13
 <211> 978
 <212> DNA

MBI-0021.txt

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (219)..(452)

<223> G1842.6

<400> 13

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tctctatcgt ctaacaaaaa aaaaaactga cttgggattt tttttcattt gtctagccca      120
aaagaagaag atagaaacga agaaaaaaag caaacacatt ttgggtcccc ggtggttagg      180
atcaaattag ggcacaaaacc ttatcggaga aagaagcc atg gga aga aga aaa gtc      236
                               Met Gly Arg Arg Lys Val
                               1           5

gag atc aag cga atc gag aac aaa agc agt cga caa gtc act ttc tcc      284
Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg Gln Val Thr Phe Ser
                10                15                20

aaa cga cgc aaa ggt ctc atc gaa aaa gct cga caa ctt tca att ctc      332
Lys Arg Arg Lys Gly Leu Ile Glu Lys Ala Arg Gln Leu Ser Ile Leu
                25                30                35

tgt gaa tct tcc atc gct gtt gtc gcc gtc tcc ggt tcc gga aaa ctc      380
Cys Glu Ser Ser Ile Ala Val Val Ala Val Ser Gly Ser Gly Lys Leu
                40                45                50

tac gac tct gcc tcc ggt gac aag atc ttg cag aaa aaa ttc gga att      428
Tyr Asp Ser Ala Ser Gly Asp Lys Ile Leu Gln Lys Lys Phe Gly Ile
55                60                65                70

atc ttc cac aca agg agt tac tag aaatagtcca aagattctct aatatctatg      482
Ile Phe His Thr Arg Ser Tyr
                75

gaggaacagc tcgagactgc tctgtcagta attagagcta agaagacaga actaatgatg      542
gaggatatga agtcacttca agaaagggag aagttgctga tagaagagaa ccagattctg      602
gctagccagg tggggaagaa gacgtttctg gttatagaag gtgacagagg aatgtcacgg      662
gaaaatggct ccggcaacaa agtaccggag actctttcgc tgctcaagta atcaccatca      722
tcaacggctg agctttcacc ataaacttac tcacagcctg attcagaagc ttttacaaaa      782
ttgtaaatta taaaaagctg cataataatc tcaacctttt tatcttcctc gcgccaatgt      842
ggaaataaag gtaaaacaaa acgaagctct tttcttttat gcgaaagaat tgtaaaacta      902
agataaagct accgatcttt gttgtacctt agtagacaaa tatcagagtt cttgtgcttg      962
aaaaaaaaaa aaaaaa                                         978

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<210> 14

<211> 77

<212> PRT

<213> Arabidopsis thaliana

MBI-0021.txt

<400> 14

Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Val Ala Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Asp Ser Ala Ser Gly Asp Lys Ile Leu
 50 55 60

Gln Lys Lys Phe Gly Ile Ile Phe His Thr Arg Ser Tyr
 65 70 75

<210> 15

<211> 876

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (80)..(436)

<223> G1842.7

<400> 15

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cttatcggag aaagaagcc atg gga aga aga aaa gtc gag atc aag cga atc 112
 Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile
 1 5 10

gag aac aaa agc agt cga caa gtc act ttc tcc aaa cga cgc aaa ggt 160
 Glu Asn Lys Ser Ser Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly
 15 20 25

ctc atc gaa aaa gct cga caa ctt tca att ctc tgt gaa tct tcc atc 208
 Leu Ile Glu Lys Ala Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile
 30 35 40

gct gtt gtc gcc gtc tcc ggt tcc gga aaa ctc tac gac tct gcc tcc 256
 Ala Val Val Ala Val Ser Gly Ser Gly Lys Leu Tyr Asp Ser Ala Ser
 45 50 55

ggt gac aac atg tca aag atc att gat cgt tat gaa ata cat cat gct 304
 Gly Asp Asn Met Ser Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala
 60 65 70 75

gat gaa ctt aaa gcc tta gat ctt gca gaa aaa att cgg aat tat ctt 352
 Asp Glu Leu Lys Ala Leu Asp Leu Ala Glu Lys Ile Arg Asn Tyr Leu
 80 85 90

cca cac aag gag tta cta gaa ata gtc caa aga ttc tct aat atc tat 400
 Pro His Lys Glu Leu Leu Glu Ile Val Gln Arg Phe Ser Asn Ile Tyr
 95 100 105

MBI-0021.txt

gga gga aca gct cga gac tgc tct gtc agt aat tag agctaagaag 446
 Gly Gly Thr Ala Arg Asp Cys Ser Val Ser Asn
 110 115

acagaactaa tgatggagga tatgaagtca cttcaagaaa gggagaagtt gctgatagaa 506
 gagaaccaga ttctggctag ccaggtgggg aagaagacgt ttctggttat agaaggtgac 566
 agaggaatgt caccgggaaaa tggtccggc aacaaagtac cggagactct ttcgctgctc 626
 aagtaatcac catcatcaac ggctgagctt tcaccataaa cttactcaca gcctgattca 686
 gaagctttta caaaattgta aattataaaa agctgcataa taatctcaac ctttttatct 746
 tcctcgcgcc aatgtggaaa taaaggtaaa acaaaacgaa gctcttttct tttatgcgaa 806
 agaattgtaa aactaagata aagctaccga tctttgttgt accttagtag acaaatatca 866
 gagttcttgt 876

<210> 16
 <211> 118
 <212> PRT
 <213> Arabidopsis thaliana

<400> 16

Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Ile Ala Val Val Ala Val
 35 40 45

Ser Gly Ser Gly Lys Leu Tyr Asp Ser Ala Ser Gly Asp Asn Met Ser
 50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile His His Ala Asp Glu Leu Lys Ala
 65 70 75 80

Leu Asp Leu Ala Glu Lys Ile Arg Asn Tyr Leu Pro His Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Arg Phe Ser Asn Ile Tyr Gly Gly Thr Ala Arg
 100 105 110

Asp Cys Ser Val Ser Asn
 115

<210> 17
 <211> 818

MBI-0021.txt

Thr Leu Leu Leu Leu Lys
195 200

aaaaattgta aaaattatga tttgtagttc ataaggaaag ctacatactg tatgttaaaa 743
atcctcttct tccccctgct acggaaaagt catccaagga gatgcatcaa ataaagtaat 803
tgatttttat tgtta 818

<210> 18
<211> 200
<212> PRT
<213> Arabidopsis thaliana

<400> 18

Met Gly Arg Arg Lys Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1 5 10 15

Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Met Glu Lys Ala
20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Leu Ile Ile Ile
35 40 45

Ser Ala Thr Gly Arg Leu Tyr Ser Phe Ser Ser Gly Asp Ser Met Ala
50 55 60

Lys Ile Leu Ser Arg Tyr Glu Leu Glu Gln Ala Asp Asp Leu Lys Thr
65 70 75 80

Leu Asp Leu Glu Glu Lys Thr Leu Asn Tyr Leu Ser His Lys Glu Leu
85 90 95

Leu Glu Thr Ile Gln Cys Lys Ile Glu Glu Ala Lys Ser Asp Asn Val
100 105 110

Ser Ile Asp Cys Leu Lys Ser Leu Glu Glu Gln Leu Lys Thr Ala Leu
115 120 125

Ser Val Thr Arg Ala Arg Lys Thr Glu Leu Met Met Glu Leu Val Lys
130 135 140

Thr His Gln Glu Lys Glu Lys Leu Leu Arg Glu Glu Asn Gln Ser Leu
145 150 155 160

Thr Asn Gln Leu Ile Lys Met Gly Lys Met Lys Lys Ser Val Glu Ala
165 170 175

Glu Asp Ala Arg Ala Met Ser Pro Glu Ser Ser Ser Asp Asn Lys Pro
180 185 190

MBI-0021.txt

Pro Glu Thr Leu Leu Leu Leu Lys
195 200

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<210> 19
<211> 834
<212> DNA
<213> Arabidopsis thaliana
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<220>  
<221> CDS  
<222> (39) .. (635)  
<223> G1844
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<400> 19
agaaattagg ggattagatg tgtcggaaga gtgaagcc atg gga aga aga aga gta      56
                               Met Gly Arg Arg Arg Val
                               1           5
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gag atc aaa cga att gag aac aaa agc agt aga caa gtc act ttc tgt 104
Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg Gln Val Thr Phe Cys
10 15 20

aag aga cga aat ggt ctc atg gag aaa gct cgt caa ctc tca att ctc 152
 Lys Arg Arg Asn Gly Leu Met Glu Lys Ala Arg Gln Leu Ser Ile Leu
 25 30 35

tgt gga tcc tcc gtc gct ctt ttc atc gtc tct tcc acc ggc aaa ctc 200
Cys Gly Ser Ser Val Ala Leu Phe Ile Val Ser Ser Thr Gly Lys Leu
40 45 50

tac	aac	tcc	tcc	tcc	ggc	gac	agc	atg	gcc	aag	atc	atc	agt	cgt	ttt	248
Tyr	Asn	Ser	Ser	Ser	Gly	Asp	Ser	Met	Ala	Lys	Ile	Ile	Ser	Arg	Phe	
55					60					65					70	

aaa ata caa caa gct gat gat cct gaa acc ttg gat ctt gaa gac aaa 296
Lys Ile Gln Gln Ala Asp Asp Pro Glu Thr Leu Asp Leu Glu Asp Lys
75 80 85

act cag gat tat ctt tca cac aag gag tta cta gaa ata gtt caa aga 344
Thr Gln Asp Tyr Leu Ser His Lys Glu Leu Leu Glu Ile Val Gln Arg
90 95 100

aag att gaa gaa gca aaa ggg gat aat gta agt ata gaa tct cta att 392
Lys Ile Glu Glu Ala Lys Gly Asp Asn Val Ser Ile Glu Ser Leu Ile
105 110 115

tcc atg gaa gag cag ctc aag agt gct ctg tct gta att aga gct agg 440
Ser Met Glu Glu Gln Leu Lys Ser Ala Leu Ser Val Ile Arg Ala Arg
120 125 130

aag aca gag tta ttg atg gag ctt gtg aag aac ctt cag gat aag gag 488
Lys Thr Glu Leu Leu Met Glu Leu Val Lys Asn Leu Gln Asp Lys Glu
135 140 145 150

aag ttg ctg aaa gaa aag aac aag gtt cta gct agc gag gtg ggg aag 536
Lys Leu Leu Lys Glu Lys Asn Lys Val Leu Ala Ser Glu Val Gly Lys
155 160 165

ctg aag aaa att ttg gaa aca ggg gat gaa aga gca gta atg tca ccg 584

MBI-0021.txt

```

Leu Lys Lys Ile Leu Glu Thr Gly Asp Glu Arg Ala Val Met Ser Pro
    170                      175                      180
gaa aat agc tct ggc cac agc cca ccg gag act ctc ccg ctt ctc aag      632
Glu Asn Ser Ser Gly His Ser Pro Pro Glu Thr Leu Pro Leu Leu Lys
    185                      190                      195
taa ccaccaatca tcaacggctg atttttcatc atcctgattc aaaaaaggta      685
aaaaaaattc atgtgtaaaa atcataaaga agctacatgt tttaaaatcc ttttctcccc      745
ctgcatacgg ataaatttat agaccaaaaa tataatgttt tccctcaaat aagatatcga      805
cctttgtgtt accttggaag acaggatca      834

```

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<210> 20
<211> 198
<212> PRT
<213> Arabidopsis thaliana
<400> 20

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Met Gly Arg Arg Arg Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1                      5                      10                      15

Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Met Glu Lys Ala
    20                      25                      30

Arg Gln Leu Ser Ile Leu Cys Gly Ser Ser Val Ala Leu Phe Ile Val
    35                      40                      45

Ser Ser Thr Gly Lys Leu Tyr Asn Ser Ser Ser Gly Asp Ser Met Ala
    50                      55                      60

Lys Ile Ile Ser Arg Phe Lys Ile Gln Gln Ala Asp Asp Pro Glu Thr
    65                      70                      75                      80

Leu Asp Leu Glu Asp Lys Thr Gln Asp Tyr Leu Ser His Lys Glu Leu
    85                      90                      95

Leu Glu Ile Val Gln Arg Lys Ile Glu Glu Ala Lys Gly Asp Asn Val
    100                      105                      110

Ser Ile Glu Ser Leu Ile Ser Met Glu Glu Gln Leu Lys Ser Ala Leu
    115                      120                      125

Ser Val Ile Arg Ala Arg Lys Thr Glu Leu Leu Met Glu Leu Val Lys
    130                      135                      140

Asn Leu Gln Asp Lys Glu Lys Leu Leu Lys Glu Lys Asn Lys Val Leu
    145                      150                      155                      160

```

MBI-0021.txt

Ala Ser Glu Val Gly Lys Leu Lys Lys Ile Leu Glu Thr Gly Asp Glu
 165 170 175

Arg Ala Val Met Ser Pro Glu Asn Ser Ser Gly His Ser Pro Pro Glu
 180 185 190

Thr Leu Pro Leu Leu Lys
 195

<210> 21
 <211> 753
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1) .. (555)
 <223> G1844.2

<400> 21
 atg gga aga aga aga gta gag atc aaa cga att gag aac aaa agc agt 48
 Met Gly Arg Arg Arg Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15
 aga caa gtc act ttc tgt aag aga cga aat ggt ctc atg gag aaa gct 96
 Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Met Glu Lys Ala
 20 25 30
 cgt caa ctc tca att ctc tgt gga tcc tcc gtc gct ctt ttc atc gtc 144
 Arg Gln Leu Ser Ile Leu Cys Gly Ser Ser Val Ala Leu Phe Ile Val
 35 40 45
 tct tcc acc ggc aaa ctc tac aac tcc tcc tcc ggc gac agc atg gcc 192
 Ser Ser Thr Gly Lys Leu Tyr Asn Ser Ser Ser Gly Asp Ser Met Ala
 50 55 60
 aag atc atc agt cgt ttt aaa ata caa caa gct gat gat cct gaa acc 240
 Lys Ile Ile Ser Arg Phe Lys Ile Gln Gln Ala Asp Asp Pro Glu Thr
 65 70 75 80
 ttg gat ctt gaa gac aaa act cag gat tat ctt tca cac aag gag tta 288
 Leu Asp Leu Glu Asp Lys Thr Gln Asp Tyr Leu Ser His Lys Glu Leu
 85 90 95
 cta gaa ata gtt caa aga aag att gaa gaa gca aaa ggg gat aat gta 336
 Leu Glu Ile Val Gln Arg Lys Ile Glu Glu Ala Lys Gly Asp Asn Val
 100 105 110
 agt ata gaa tct cta att tcc atg gaa gag cag ctc aag agt gct ctg 384
 Ser Ile Glu Ser Leu Ile Ser Met Glu Glu Gln Leu Lys Ser Ala Leu
 115 120 125
 tct gta att aga gct agg aag aca gag tta ttg atg gag ctt gtg aag 432
 Ser Val Ile Arg Ala Arg Lys Thr Glu Leu Leu Met Glu Leu Val Lys
 130 135 140
 aac ctt cag gat aag gtg ggg aag ctg aag aaa att ttg gaa aca ggg 480
 Asn Leu Gln Asp Lys Val Gly Lys Leu Lys Lys Ile Leu Glu Thr Gly
 145 150 155 160

MBI-0021.txt

gat gaa aga gca gta atg tca ccg gaa aat agc tct ggc cac agc cca 528
 Asp Glu Arg Ala Val Met Ser Pro Glu Asn Ser Ser Gly His Ser Pro
 165 170 175

ccg gag act ctc ccg ctt ctc aag taa ccaccaatca tcaacggctg 575
 Pro Glu Thr Leu Pro Leu Leu Lys
 180

atttttcatc atcctgattc aaaaaaggta aaaaaaatc atgtgtaaaa atcataaaga 635

agctacatgt tttaaaatcc ttttctcccc ctgcatacgg ataaatttat agaccaaaaa 695

tataatgttt tccctcaa ataatatcga cctttgtgtt accttggaag acaggatc 753

<210> 22

<211> 184

<212> PRT

<213> Arabidopsis thaliana

<400> 22

Met Gly Arg Arg Arg Val Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Met Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Ile Leu Cys Gly Ser Ser Val Ala Leu Phe Ile Val
 35 40 45

Ser Ser Thr Gly Lys Leu Tyr Asn Ser Ser Ser Gly Asp Ser Met Ala
 50 55 60

Lys Ile Ile Ser Arg Phe Lys Ile Gln Gln Ala Asp Asp Pro Glu Thr
 65 70 75 80

Leu Asp Leu Glu Asp Lys Thr Gln Asp Tyr Leu Ser His Lys Glu Leu
 85 90 95

Leu Glu Ile Val Gln Arg Lys Ile Glu Glu Ala Lys Gly Asp Asn Val
 100 105 110

Ser Ile Glu Ser Leu Ile Ser Met Glu Glu Gln Leu Lys Ser Ala Leu
 115 120 125

Ser Val Ile Arg Ala Arg Lys Thr Glu Leu Leu Met Glu Leu Val Lys
 130 135 140

Asn Leu Gln Asp Lys Val Gly Lys Leu Lys Lys Ile Leu Glu Thr Gly
 145 150 155 160

MBI-0021.txt

Asp Glu Arg Ala Val Met Ser Pro Glu Asn Ser Ser Gly His Ser Pro
165 170 175

Pro Glu Thr Leu Pro Leu Leu Lys
180

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<210> 23
<211> 1134
<212> DNA
<213> Arabidopsis thaliana
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<220>
<221> CDS
<222> (158) .. (880)
<223> G861
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<400> 23																
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atcttgatcc	atcaaaatca	atcccgtttc	cgaaagatcc	attaaaaatca	aaacctaagc											120
tctctctctt	gcttctaggg	tttttttggt	cgttgtg	atg	gcg	aga	gaa	aag	att							175
				Met	Ala	Arg	Glu	Lys	Ile							
				1				5								
cag	atc	agg	aag	atc	gac	aac	gca	acg	gcg	aga	caa	gtg	acg	ttt	tcg	223
Gln	Ile	Arg	Lys	Ile	Asp	Asn	Ala	Thr	Ala	Arg	Gln	Val	Thr	Phe	Ser	
			10					15					20			
aaa	cga	aga	aga	ggg	ctt	ttc	aag	aaa	gct	gaa	gaa	ctc	tcc	gtt	ctc	271
Lys	Arg	Arg	Arg	Gly	Leu	Phe	Lys	Lys	Ala	Glu	Glu	Leu	Ser	Val	Leu	
			25				30					35				
tgc	gac	gcc	gat	gtc	gct	ctc	atc	atc	ttc	tct	tcc	acc	gga	aaa	ctg	319
Cys	Asp	Ala	Asp	Val	Ala	Leu	Ile	Ile	Phe	Ser	Ser	Thr	Gly	Lys	Leu	
			40			45					50					
ttc	gag	ttc	tgt	agc	tcc	agc	atg	aag	gaa	gtc	cta	gag	agg	cat	aac	367
Phe	Glu	Phe	Cys	Ser	Ser	Ser	Met	Lys	Glu	Val	Leu	Glu	Arg	His	Asn	
55					60					65					70	
ttg	cag	tca	aag	aac	ttg	gag	aag	ctt	gat	cag	cca	tct	ctt	gag	tta	415
Leu	Gln	Ser	Lys	Asn	Leu	Glu	Lys	Leu	Asp	Gln	Pro	Ser	Leu	Glu	Leu	
				75				80						85		
cag	ctg	gtt	gag	aac	agt	gat	cac	gcc	cga	atg	agt	aaa	gaa	att	gcg	463
Gln	Leu	Val	Glu	Asn	Ser	Asp	His	Ala	Arg	Met	Ser	Lys	Glu	Ile	Ala	
			90					95					100			
gac	aag	agc	cac	cga	cta	agg	caa	atg	aga	gga	gag	gaa	ctt	caa	gga	511
Asp	Lys	Ser	His	Arg	Leu	Arg	Gln	Met	Arg	Gly	Glu	Glu	Leu	Gln	Gly	
			105				110					115				
ctt	gac	att	gaa	gag	ctt	cag	cag	cta	gag	aag	gcc	ctt	gaa	act	ggt	559
Leu	Asp	Ile	Glu	Glu	Leu	Gln	Gln	Leu	Glu	Lys	Ala	Leu	Glu	Thr	Gly	
			120			125					130					
ttg	acg	cgt	gtg	att	gaa	aca	aag	agt	gac	aag	att	atg	agt	gag	atc	607
Leu	Thr	Arg	Val	Ile	Glu	Thr	Lys	Ser	Asp	Lys	Ile	Met	Ser	Glu	Ile	
135					140					145					150	

MBI-0021.txt

```

agc gaa ctt cag aaa aag gga atg caa ttg atg gat gag aac aag cgg      655
Ser Glu Leu Gln Lys Lys Gly Met Gln Leu Met Asp Glu Asn Lys Arg
      155      160      165

ttg agg cag caa gga acg caa cta acg gaa gag aac gag cga ctt ggc      703
Leu Arg Gln Gln Gly Thr Gln Leu Thr Glu Glu Asn Glu Arg Leu Gly
      170      175      180

atg caa ata tgt aac aat gtg cat gca cac ggt ggt gct gaa tcg gag      751
Met Gln Ile Cys Asn Asn Val His Ala His Gly Gly Ala Glu Ser Glu
      185      190      195

aac gct gct gtg tac gag gaa gga cag tcg tcg gag tct att act aac      799
Asn Ala Ala Val Tyr Glu Glu Gly Gln Ser Ser Glu Ser Ile Thr Asn
      200      205      210

gcc gga aac tct acc gga gcg cct gtt gac tcc gag agc tcc gac act      847
Ala Gly Asn Ser Thr Gly Ala Pro Val Asp Ser Glu Ser Ser Asp Thr
      215      220      225      230

tcc ctt agg ctc ggc tta ccg tat ggt ggt tag agatggaaca attcaaagaa      900
Ser Leu Arg Leu Gly Leu Pro Tyr Gly Gly
      235      240

gttgatggag tgaggagagt aatgtaaadc tttttaactc ggtagtaaca agagacaatg      960

tctaagtagt gaattctcaa atgtttgtgt aagtttctgc ctatggaaga ggctttcatt      1020

tttatgattt tcaactatgta tgatctctct tcaactgcatt tctggttagt aacggcttgt      1080

caccgataaa ctttctcggt atggaaagtt agaataaaaa aaaaaaaaaa aaaa      1134

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<210> 24
<211> 240
<212> PRT
<213> Arabidopsis thaliana

<400> 24

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Met Ala Arg Glu Lys Ile Gln Ile Arg Lys Ile Asp Asn Ala Thr Ala
1      5      10      15

```

```

Arg Gln Val Thr Phe Ser Lys Arg Arg Arg Gly Leu Phe Lys Lys Ala
      20      25      30

```

```

Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe
      35      40      45

```

```

Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser Met Lys Glu
      50      55      60

```

```

Val Leu Glu Arg His Asn Leu Gln Ser Lys Asn Leu Glu Lys Leu Asp
      65      70      75      80

```

```

Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp His Ala Arg
      85      90      95

```

MBI-0021.txt

Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg Gln Met Arg
 100 105 110

Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln Gln Leu Glu
 115 120 125

Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr Lys Ser Asp
 130 135 140

Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly Met Gln Leu
 145 150 155 160

Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Gly Thr Gln Leu Thr Glu
 165 170 175

Glu Asn Glu Arg Leu Gly Met Gln Ile Cys Asn Asn Val His Ala His
 180 185 190

Gly Gly Ala Glu Ser Glu Asn Ala Ala Val Tyr Glu Glu Gly Gln Ser
 195 200 205

Ser Glu Ser Ile Thr Asn Ala Gly Asn Ser Thr Gly Ala Pro Val Asp
 210 215 220

Ser Glu Ser Ser Asp Thr Ser Leu Arg Leu Gly Leu Pro Tyr Gly Gly
 225 230 235 240

<210> 25
 <211> 1552
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (193)..(825)
 <223> G861.1

<400> 25
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 tctttactct ctctttaatc atctctcatt cttgaatctt gatccatcaa aatcaatccc 120
 gttctcgaaa gatccattaa aatcaaaacc taagctctct ctcttgcttc tagggttttt 180
 ttgttcgttg tg atg gcg aga gaa aag att cag atc agg aag atc gac aac 231
 Met Ala Arg Glu Lys Ile Gln Ile Arg Lys Ile Asp Asn
 1 5 10
 gca acg gcg aga caa gtg acg ttt tcg aaa cga aga aga ggg ctt ttc 279
 Ala Thr Ala Arg Gln Val Thr Phe Ser Lys Arg Arg Arg Gly Leu Phe
 15 20 25

MBI-0021.txt

```

aag aaa gct gaa gaa ctc tcc gtt ctc tgc gac gcc gat gtc gct ctc      327
Lys Lys Ala Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu
30                      35                      40                      45

atc atc ttc tct tcc acc gga aaa ctg ttc gag ttc tgt agc tcc agc      375
Ile Ile Phe Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser
50                      55                      60

atg aag gaa gtc cta gag agg cat aac ttg cag tca aag aac ttg gag      423
Met Lys Glu Val Leu Glu Arg His Asn Leu Gln Ser Lys Asn Leu Glu
65                      70                      75

aag ctt gat cag cca tct ctt gag tta cag ctg gtt gag aac agt gat      471
Lys Leu Asp Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp
80                      85                      90

cac gcc cga atg agt aaa gaa att gcg gac aag agc cac cga cta agg      519
His Ala Arg Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg
95                      100                      105

caa atg aga gga gag gaa ctt caa gga ctt gac att gaa gag ctt cag      567
Gln Met Arg Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln
110                      115                      120                      125

cag cta gag aag gcc ctt gaa act ggt ttg acg cgt gtg att gaa aca      615
Gln Leu Glu Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr
130                      135                      140

aag agt gac aag att atg agt gag atc agc gaa ctt cag aaa aag gga      663
Lys Ser Asp Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly
145                      150                      155

atg caa ttg atg gat gag aac aag cgg ttg agg cag caa gta tgt gtc      711
Met Gln Leu Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Val Cys Val
160                      165                      170

tta ccc tct ctg ttg ata aca aat ccc ttt ctt ttg tct acc att aac      759
Leu Pro Ser Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn
175                      180                      185

gta cac act cct aaa ttt aat ccc cag ttg tct aca aca cat atg ttt      807
Val His Thr Pro Lys Phe Asn Pro Gln Leu Ser Thr Thr His Met Phe
190                      195                      200                      205

gat cat act gtg aga taa atgaataaac caagtgatat agcgcgattt      855
Asp His Thr Val Arg
210

aaaaatgtct ttaaaactaa aggtaaccat gtagctagtt agtctctagg gtcctagagg      915

tctacgagtg tgcatgcatg gatttggtgc gttttttctt tttcatcttc attttgtttt      975

ttgaaacaag gaaccataaa cgaatatata tctaattctt gtttgatata tagtttggtc      1035

gaggcttcat gtcaagattt gctcattcgt agttagttga tctctagaga aattcaaaac      1095

acatggtgcc actaaaaaca caaatgcaa atacttagct agagaactta atgatatggt      1155

ttgtcttgat ttttgcaggg aacgcaacta acggaagaga acgagcgact tggcatgcaa      1215

atatgtaaca atgtgcatgc acacggtggt gctgaatcgg agaacgctgc tgtgtacgag      1275

```

MBI-0021.txt

```

gaaggacagt cgtcggagtc tattactaac gccggaaact ctaccggagc gcctgttgac 1335
tccgagagct ccgacacttc ccttaggctc ggcttaccgt atgggtggta gagatggaac 1395
aattcaaaga agttgatgga gtgaggagag taatgtaaat ctttttaact cggtagtaac 1455
aagagacaat gtctaagtag tgaattctca aatgtttgtg taagtttctg cctatggaag 1515
aggctttcat ttttatgatt aaaaaaaaaa aaaaaaa 1552

```

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<210> 26
<211> 210
<212> PRT
<213> Arabidopsis thaliana

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<400> 26

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Met Ala Arg Glu Lys Ile Gln Ile Arg Lys Ile Asp Asn Ala Thr Ala
1          5          10          15

```

```

Arg Gln Val Thr Phe Ser Lys Arg Arg Arg Gly Leu Phe Lys Lys Ala
          20          25          30

```

```

Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe
35          40          45

```

```

Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser Met Lys Glu
50          55          60

```

```

Val Leu Glu Arg His Asn Leu Gln Ser Lys Asn Leu Glu Lys Leu Asp
65          70          75          80

```

```

Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp His Ala Arg
85          90          95

```

```

Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg Gln Met Arg
100          105          110

```

```

Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln Gln Leu Glu
115          120          125

```

```

Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr Lys Ser Asp
130          135          140

```

```

Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly Met Gln Leu
145          150          155          160

```

```

Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Val Cys Val Leu Pro Ser
165          170          175

```

```

Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn Val His Thr

```

MBI-0021.txt

180

185

190

Pro Lys Phe Asn Pro Gln Leu Ser Thr Thr His Met Phe Asp His Thr
 195 200 205

Val Arg
 210

<210> 27
 <211> 943
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (110)..(700)
 <223> G1759

<400> 27
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 ccaaacctga ggatcaaatt agggcacaaa gccctctcgg agagaagcc atg gga aga 118
 Met Gly Arg
 1
 aaa aaa cta gaa atc aag cga att gag aac aaa agt agc cga caa gtc 166
 Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg Gln Val
 5 10 15
 acc ttc tcc aaa cgt cgc aac ggt ctc atc gag aaa gct cgt cag ctt 214
 Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala Arg Gln Leu
 20 25 30 35
 tct gtt ctc tgt gac gca tcc gtc gct ctt ctc gtc gtc tcc gcc tcc 262
 Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val Ser Ala Ser
 40 45 50
 ggc aag ctc tac agc ttc tcc tcc ggc gat aac ctg gtc aag atc ctt 310
 Gly Lys Leu Tyr Ser Phe Ser Ser Gly Asp Asn Leu Val Lys Ile Leu
 55 60 65
 gat cga tat ggg aaa cag cat gct gat gat ctt aaa gcc ttg gat cat 358
 Asp Arg Tyr Gly Lys Gln His Ala Asp Asp Leu Lys Ala Leu Asp His
 70 75 80
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 Gln Ser Lys Ala Leu Asn Tyr Gly Ser His Tyr Glu Leu Leu Glu Leu
 85 90 95
 gtg gat agc aag ctt gtg gga tca aat gtc aaa aat gtg agt atc gat 454
 Val Asp Ser Lys Leu Val Gly Ser Asn Val Lys Asn Val Ser Ile Asp
 100 105 110 115
 gct ctt gtt caa ctg gag gaa cac ctt gag act gcc ctc tcc gtg act 502
 Ala Leu Val Gln Leu Glu Glu His Leu Glu Thr Ala Leu Ser Val Thr
 120 125 130
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 Arg Ala Lys Lys Thr Glu Leu Met Leu Lys Leu Val Glu Asn Leu Lys

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135	140	145	
gaa aag gag aaa atg ctg aaa	gaa gag aac cag gtt ttg gct agc cag		598
Glu Lys Glu Lys Met Leu Lys	Glu Glu Asn Gln Val Leu Ala Ser Gln		
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Met Glu Asn Asn His His Val Gly Ala Glu Ala Glu Met Glu Met Ser			
165	170 175		
cct gct gga caa atc tcc gac aat ctt ccg gtg act ctc cca cta ctt			694
Pro Ala Gly Gln Ile Ser Asp Asn Leu Pro Val Thr Leu Pro Leu Leu			
180	185 190 195		
aat tag ccaccttaaa tcggcggttg aaatcaaaat ccaaaacata tataattatg			750
Asn			
aagaaaaaaaa aaataagata tgtaattatt ccgctgataa gggcgagcgt ttgtatatct			810
taataactctc tctttggcca agagactttg tgtgtgatac ttaagtagac ggaactaagt			870
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Ser Ala Ser Gly Lys Leu Tyr Ser Phe Ser Ser Gly Asp Asn Leu Val			
50 55 60			
Lys Ile Leu Asp Arg Tyr Gly Lys Gln His Ala Asp Asp Leu Lys Ala			
65 70 75 80			
Leu Asp His Gln Ser Lys Ala Leu Asn Tyr Gly Ser His Tyr Glu Leu			
85 90 95			
Leu Glu Leu Val Asp Ser Lys Leu Val Gly Ser Asn Val Lys Asn Val			
100 105 110			
Ser Ile Asp Ala Leu Val Gln Leu Glu Glu His Leu Glu Thr Ala Leu			

MBI-0021.txt

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115                               120                               125

Ser Val Thr Arg Ala Lys Lys Thr Glu Leu Met Leu Lys Leu Val Glu
130                               135                               140

Asn Leu Lys Glu Lys Glu Lys Met Leu Lys Glu Glu Asn Gln Val Leu
145                               150                               155                               160

Ala Ser Gln Met Glu Asn Asn His His Val Gly Ala Glu Ala Glu Met
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Glu Met Ser Pro Ala Gly Gln Ile Ser Asp Asn Leu Pro Val Thr Leu
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Pro Leu Leu Asn
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  Met Ala Asp Asp Trp Asp Leu His Ala Val Val Arg Gly Cys Ser
    1                               5                               10                               15

gcc gta agc tca tca gct act acc acc gta tat tcc ccc ggc gtt tca      155
Ala Val Ser Ser Ser Ala Thr Thr Thr Val Tyr Ser Pro Gly Val Ser
                               20                               25                               30

tct cac aca aac cct ata ttc acc gtc gga cga caa agt aat gcc gtc      203
Ser His Thr Asn Pro Ile Phe Thr Val Gly Arg Gln Ser Asn Ala Val
                               35                               40                               45

tcc ttc gga gag att cga gat ctc tac aca ccg ttc aca caa gaa tct      251
Ser Phe Gly Glu Ile Arg Asp Leu Tyr Thr Pro Phe Thr Gln Glu Ser
    50                               55                               60

gtc gtc tct tcg ttt tct tgt ata aac tac cca gaa gaa cct aga aag      299
Val Val Ser Ser Phe Ser Cys Ile Asn Tyr Pro Glu Glu Pro Arg Lys
    65                               70                               75

cca cag aac cag aaa cgt cct ctt tct ctc tct gct tct tcc ggt agc      347
Pro Gln Asn Gln Lys Arg Pro Leu Ser Leu Ser Ala Ser Ser Gly Ser
    80                               85                               90                               95

gtc act agc aaa ccc agt ggc tcc aat acc tct aga tct aaa aga aga      395
Val Thr Ser Lys Pro Ser Gly Ser Asn Thr Ser Arg Ser Lys Arg Arg
                               Page 30

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MBI-0021.txt

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Ser Asp Val Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly			
130	135	140	
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Ser Pro Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser Thr Ser Lys Gly Cys			
145	150	155	
tta gcc cgt aaa caa gtg gag cga aat aga tcc gac ccg aag atg ttt			587
Leu Ala Arg Lys Gln Val Glu Arg Asn Arg Ser Asp Pro Lys Met Phe			
160	165	170	175
atc gtc act tac acg gcg gag cat aat cat cca gct ccg aca cac cgt			635
Ile Val Thr Tyr Thr Ala Glu His Asn His Pro Ala Pro Thr His Arg			
180	185	190	
aat tct ctc gcc gga agc aca cgt cag aaa cca tcc gat caa cag acg			683
Asn Ser Leu Ala Gly Ser Thr Arg Gln Lys Pro Ser Asp Gln Gln Thr			
195	200	205	
agt aaa tct ccg acg acc act att gct act tat tca tcg tct ccg gtg			731
Ser Lys Ser Pro Thr Thr Thr Ile Ala Thr Tyr Ser Ser Ser Pro Val			
210	215	220	
act tca gcc gac gaa ttt gtt ttg cct gtt gag gat cat cta gcg gtg			779
Thr Ser Ala Asp Glu Phe Val Leu Pro Val Glu Asp His Leu Ala Val			
225	230	235	
gga gat ctt gac gga gaa gaa gat ctg tta tct ttg tcg gat acg gtg			827
Gly Asp Leu Asp Gly Glu Glu Asp Leu Leu Ser Leu Ser Asp Thr Val			
240	245	250	255
gtt agc gat gat ttc ttc gat ggg tta gag gaa ttc gca gcc gga gat			875
Val Ser Asp Asp Phe Phe Asp Gly Leu Glu Glu Phe Ala Ala Gly Asp			
260	265	270	
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Ser Phe Ser Gly Asn Ser Ala Pro Ala Ser Phe Asp Leu Ser Trp Val			
275	280	285	
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Val Asn Ser Ala Ala Thr Thr Thr Gly Gly Ile			
290	295		
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tatgtaaaaa taggataaaaa gaaaatgttc ttgttactt tttttcgggt tttcttccta			1089
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MBI-0021.txt

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35 40 45

Phe Gly Glu Ile Arg Asp Leu Tyr Thr Pro Phe Thr Gln Glu Ser Val
50 55 60

Val Ser Ser Phe Ser Cys Ile Asn Tyr Pro Glu Glu Pro Arg Lys Pro
65 70 75 80

Gln Asn Gln Lys Arg Pro Leu Ser Leu Ser Ala Ser Ser Gly Ser Val
85 90 95

Thr Ser Lys Pro Ser Gly Ser Asn Thr Ser Arg Ser Lys Arg Arg Lys
100 105 110

Ile Gln His Lys Lys Val Cys His Val Ala Ala Glu Ala Leu Asn Ser
115 120 125

Asp Val Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser
130 135 140

Pro Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser Thr Ser Lys Gly Cys Leu
145 150 155 160

Ala Arg Lys Gln Val Glu Arg Asn Arg Ser Asp Pro Lys Met Phe Ile
165 170 175

Val Thr Tyr Thr Ala Glu His Asn His Pro Ala Pro Thr His Arg Asn
180 185 190

Ser Leu Ala Gly Ser Thr Arg Gln Lys Pro Ser Asp Gln Gln Thr Ser
195 200 205

Lys Ser Pro Thr Thr Thr Ile Ala Thr Tyr Ser Ser Ser Pro Val Thr
210 215 220

Ser Ala Asp Glu Phe Val Leu Pro Val Glu Asp His Leu Ala Val Gly
225 230 235 240

MBI-0021.txt

Asp Leu Asp Gly Glu Glu Asp Leu Leu Ser Leu Ser Asp Thr Val Val
 245 250 255

Ser Asp Asp Phe Phe Asp Gly Leu Glu Glu Phe Ala Ala Gly Asp Ser
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 275 280 285

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 Met Gly Arg Ala
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ccg tgt tgt gac aaa gca aac gtg aag aaa ggg cct tgg tct cct gag 165
 Pro Cys Cys Asp Lys Ala Asn Val Lys Lys Gly Pro Trp Ser Pro Glu
 5 10 15 20

gaa gat gca aaa ctc aaa tct tac att gaa aat agt ggc acc gga ggc 213
 Glu Asp Ala Lys Leu Lys Ser Tyr Ile Glu Asn Ser Gly Thr Gly Gly
 25 30 35

aat tgg atc gct ttg cct caa aag att ggt tta aag aga tgt gga aag 261
 Asn Trp Ile Ala Leu Pro Gln Lys Ile Gly Leu Lys Arg Cys Gly Lys
 40 45 50

agt tgc agg ctg agg tgg ctt aac tat ctt aga cca aac atc aaa cat 309
 Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asn Ile Lys His
 55 60 65

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 70 75 80

aca att ggt agc agg tgg tct ata atc gct gct caa ttg ccg gga cga 405
 Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln Leu Pro Gly Arg
 85 90 95 100

aca gac aac gat ata aaa aac tat tgg aac acg agg ctc aag aag aaa 453
 Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg Leu Lys Lys Lys
 105 110 115

ctc att aac aaa caa cgc aag gag ctt caa gaa gct tgt atg gag cag 501
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MBI-0021.txt

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Gln	Glu	Met	Met	Val	Met	Met	Lys	Arg	Gln	His	Gln	Gln	Gln	Gln	Ile		
		135					140					145					
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Gln	Thr	Ser	Phe	Met	Met	Arg	Gln	Asp	Gln	Thr	Met	Phe	Thr	Trp	Pro		
	150					155					160						
cta	cat	cat	cat	aat	gtt	caa	gtt	cca	gct	ctt	ttc	aga	atc	aaa	cca		645
Leu	His	His	His	Asn	Val	Gln	Val	Pro	Ala	Leu	Phe	Arg	Ile	Lys	Pro		
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act	cgt	ttt	gcg	acc	aag	aag	atg	tta	agc	cag	tgc	tca	tca	aga	aca		693
Thr	Arg	Phe	Ala	Thr	Lys	Lys	Met	Leu	Ser	Gln	Cys	Ser	Ser	Arg	Thr		
			185						190					195			
tgg	tca	aga	tcg	aag	atc	aag	aac	tgg	aga	aaa	caa	acc	tca	tca	tca		741
Trp	Ser	Arg	Ser	Lys	Ile	Lys	Asn	Trp	Arg	Lys	Gln	Thr	Ser	Ser	Ser		
			200					205					210				
tca	aga	ttc	aat	gac	aac	gct	ttt	gat	cat	ctc	tct	ttc	tct	caa	ctc		789
Ser	Arg	Phe	Asn	Asp	Asn	Ala	Phe	Asp	His	Leu	Ser	Phe	Ser	Gln	Leu		
		215					220					225					
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Leu	Leu	Asp	Pro	Asn	His	Asn	His	Leu	Gly	Ser	Gly	Glu	Gly	Phe	Ser		
	230					235					240						
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Met	Asn	Ser	Ile	Leu	Ser	Ala	Asn	Thr	Asn	Ser	Pro	Leu	Leu	Asn	Thr		
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agt	aat	gat	aat	cag	tgg	ttc	ggg	aat	ttc	cag	gcc	gaa	acc	gta	aac		933
Ser	Asn	Asp	Asn	Gln	Trp	Phe	Gly	Asn	Phe	Gln	Ala	Glu	Thr	Val	Asn		
			265					270						275			
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Leu	Phe	Ser	Gly	Ala	Ser	Thr	Ser	Thr	Ser	Ala	Asp	Gln	Ser	Thr	Ile		
			280				285						290				
agt	tgg	gaa	gac	ata	agc	tct	ctt	gtt	tat	tct	gat	tca	aag	caa	ttt		1029
Ser	Trp	Glu	Asp	Ile	Ser	Ser	Leu	Val	Tyr	Ser	Asp	Ser	Lys	Gln	Phe		
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MBI-0021.txt

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Phe	Thr	Trp	Pro	Leu 165	His	His	His	Asn	Val 170	Gln	Val	Pro	Ala	Leu 175	Phe
Arg	Ile	Lys	Pro 180	Thr	Arg	Phe	Ala	Thr 185	Lys	Lys	Met	Leu	Ser 190	Gln	Cys
Ser	Ser	Arg 195	Thr	Trp	Ser	Arg	Ser 200	Lys	Ile	Lys	Asn 205	Trp	Arg	Lys	Gln
Thr	Ser 210	Ser	Ser	Ser	Arg	Phe 215	Asn	Asp	Asn	Ala	Phe 220	Asp	His	Leu	Ser
Phe 225	Ser	Gln	Leu	Leu	Leu 230	Asp	Pro	Asn	His	Asn 235	His	Leu	Gly	Ser	Gly 240
Glu	Gly	Phe	Ser	Met 245	Asn	Ser	Ile	Leu	Ser 250	Ala	Asn	Thr	Asn	Ser 255	Pro
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MBI-0021.txt

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gag cgt cag ctt ctt aaa cgt gca cag atg tta gct act cgt ggt ttg			296
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85	90	95	
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Met Met Leu Ser Pro Ser Ser Ser Ser Ser Lys Trp Leu Tyr Gly Glu			
115	120	125	

MBI-0021.txt

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ctt tac gga ggt ggc atg gag tct atg gcc gga gaa gta aag act cat	536
Leu Tyr Gly Gly Gly Met Glu Ser Met Ala Gly Glu Val Lys Thr His	
150 155 160	
ggg ggt tct ttg ccg gag atg agg agg ttc gcc gga gat agt gat cgg	584
Gly Gly Ser Leu Pro Glu Met Arg Arg Phe Ala Gly Asp Ser Asp Arg	
165 170 175	
agt agc gga att aag tta gag aat ggt att ggg ctg gac ctc cat tta	632
Ser Ser Gly Ile Lys Leu Glu Asn Gly Ile Gly Leu Asp Leu His Leu	
180 185 190	
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Ser Leu Gly Pro	
195	
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Glu Phe Ala Asn Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys	
50 55 60	
Lys Glu Arg Gln Leu Leu Lys Arg Ala Gln Met Leu Ala Thr Arg Gly	
65 70 75 80	
Leu Pro Arg His His Asn Phe His Pro His Thr Asn Pro Leu Leu Ser	
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Ala Phe Ala Pro Leu Pro His Leu Leu Ser Gln Pro His Pro Pro Pro	
100 105 110	

MBI-0021.txt

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 115 120 125

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 145 150 155 160

His Gly Gly Ser Leu Pro Glu Met Arg Arg Phe Ala Gly Asp Ser Asp
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 20 25 30

caa aca gtt caa gaa tgt gca aca gag ttc ata agc ttt gtt aca tgc 144
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 35 40 45

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MBI-0021.txt

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Thr Asn Thr Arg Ser Asp Val Gln Asn Gln Ser Thr Lys Phe Ile Arg			
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Gln Thr Val Gln Glu Cys Ala Thr Glu Phe Ile Ser Phe Val Thr Cys
 35 40 45

Glu Ala Ser Glu Lys Cys His Arg Glu Asn Arg Lys Thr Val Asn Gly
 50 55 60

Asp Asp Ile Trp Trp Ala Leu Ser Thr Leu Gly Leu Asp Asn Tyr Ala
 65 70 75 80

Asp Ala Val Gly Arg His Leu His Lys Tyr Arg Glu Ala Glu Arg Glu
 85 90 95

Arg Thr Glu His Asn Lys Gly Ser Asn Asp Ser Gly Asn Glu Lys Glu
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MBI-0021.txt

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                                     Met Met Met Glu Thr Arg
                                     1                               5

gat cca gct att aag ctt ttc ggt atg aaa atc cct ttt ccg tcg gtt      163
Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile Pro Phe Pro Ser Val
                                     10                               15                               20

ttt gaa tcg gca gtt acg gtg gag gat gac gaa gaa gat gac tgg agc      211
Phe Glu Ser Ala Val Thr Val Glu Asp Asp Glu Glu Asp Asp Trp Ser
                                     25                               30                               35

ggc gga gat gac aaa tca cca gag aag gta act cca gag tta tca gat      259
Gly Gly Asp Asp Lys Ser Ser Glu Lys Val Thr Pro Glu Leu Ser Asp
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aag aac aac aac aac tgt aac gac aac agt ttt aac aat tcg aaa ccc      307
Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser Phe Asn Asn Ser Lys Pro
                                     55                               60                               65                               70

gaa acc ttg gac aaa gag gaa gcg aca tca act gat cag ata gag agt      355
Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser Thr Asp Gln Ile Glu Ser
                                     75                               80                               85

agt gac acg cct gag gat aat cag cag acg aca cct gat ggt aaa acc      403
Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr Thr Pro Asp Gly Lys Thr
                                     90                               95                               100

cta aag aaa ccg act aag att cta ccg tgt ccg aga tgc aaa agc atg      451
Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Lys Ser Met
                                     105                               110                               115

gag acc aag ttc tgt tat tac aac aac tac aac ata aac cag cct cgt      499
Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Ile Asn Gln Pro Arg
                                     120                               125                               130

cat ttc tgc aag gct tgt cag aga tat tgg act gct gga ggg act atg      547
His Phe Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ala Gly Gly Thr Met
                                     135                               140                               145                               150

agg aat gtt cct gtg ggg gca gga cgt cgt aag aac aaa agc tca tct      595
Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Asn Lys Ser Ser Ser
                                     155                               160                               165

tct cat tac cgt cac atc act att tcc gag gct ctt gag gct gcg agg      643
Ser His Tyr Arg His Ile Thr Ile Ser Glu Ala Leu Glu Ala Ala Arg
                                     170                               175                               180

ctt gac ccg ggc tta cag gca aac aca agg gtc ttg agt ttt ggt ctc      691
Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg Val Leu Ser Phe Gly Leu
                                     185                               190                               195

gaa gct cag cag cag cac gtt gct gct ccc atg aca cct gtt atg aag      739
Glu Ala Gln Gln Gln His Val Ala Ala Pro Met Thr Pro Val Met Lys
                                     200                               205                               210

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MBI-0021.txt

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	235	240	245	
tgc tca agc gga tcc tct gtg acc acc Cys Ser Ser Gly Ser Ser Val Thr Thr	tct aac aat cac tca gtg gat Ser Asn Asn His Ser Val Asp			883
	250	255	260	
gaa tca aga gca caa agc ggc agt gtt gtt gaa gca caa atg aac aac Glu Ser Arg Ala Gln Ser Gly Ser Val Val Glu Ala Gln Met Asn Asn				931
	265	270	275	
aac aac aac aat aac atg aat ggt tat gct tgc atc cca ggt gtt cca Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala Cys Ile Pro Gly Val Pro				979
	280	285	290	
tgg cct tac acg tgg aat cca gcg atg cct cca cca ggt ttt tac ccg Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro Pro Gly Phe Tyr Pro				1027
	300	305	310	
cct cca ggg tat cca atg ccg ttt tac cct tac tgg acc atc cca atg Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro Tyr Trp Thr Ile Pro Met				1075
	315	320	325	
cta cca ccg cat caa tcc tca tcg cct ata agc caa aag tgt tca aat Leu Pro Pro His Gln Ser Ser Ser Pro Ile Ser Gln Lys Cys Ser Asn				1123
	330	335	340	
aca aac tct ccg act ctc gga aag cat ccg aga gat gaa gga tca tcg Thr Asn Ser Pro Thr Leu Gly Lys His Pro Arg Asp Glu Gly Ser Ser				1171
	345	350	355	
aaa aag gac aat gag aca gag cga aaa cag aag gcc ggg tgc gtt ctg Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln Lys Ala Gly Cys Val Leu				1219
	360	365	370	
gtc ccg aaa acg ttg aga ata gat gat cct aac gaa gca gca aag agc Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu Ala Ala Lys Ser				1267
	375	380	385	
tcg ata tgg aca aca ttg gga atc aag aac gag gcg atg tgc aaa gcc Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Ala Met Cys Lys Ala				1315
	395	400	405	
ggg ggt atg ttc aaa ggg ttt gat cat aag aca aag atg tat aac aac Gly Gly Met Phe Lys Gly Phe Asp His Lys Thr Lys Met Tyr Asn Asn				1363
	410	415	420	
gac aaa gct gag aac tcc cct gtt ctt tct gct aac cct gct gct cta Asp Lys Ala Glu Asn Ser Pro Val Leu Ser Ala Asn Pro Ala Ala Leu				1411
	425	430	435	
tca aga tca cac aat ttc cat gaa cag att tag agttacatat gtatatgtat Ser Arg Ser His Asn Phe His Glu Gln Ile				1464
	440	445		
atatgtatga ttgattgtat gtatagatga tactggagaa tgatgagttt ttgagaatca				1524
aactctttttc ttcttttctag tgattgcctt tattccttta catgtttttgg ttctctgtac				1584
actattttgat ttaccttttt tactttcttt cttcatttgt caggaaatgt tggaagataa				1644

MBI-0021.txt

cattaatggt aaaaagttgg tgtggaccgt tgttgcgttg gcatttcaaa aaaaaaaaaa 1704
 aaa 1707

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 35 40 45

Thr Pro Glu Leu Ser Asp Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser
 50 55 60

Phe Asn Asn Ser Lys Pro Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser
 65 70 75 80

Thr Asp Gln Ile Glu Ser Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr
 85 90 95

Thr Pro Asp Gly Lys Thr Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys
 100 105 110

Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr
 115 120 125

Asn Ile Asn Gln Pro Arg His Phe Cys Lys Ala Cys Gln Arg Tyr Trp
 130 135 140

Thr Ala Gly Gly Thr Met Arg Asn Val Pro Val Gly Ala Gly Arg Arg
 145 150 155 160

Lys Asn Lys Ser Ser Ser Ser His Tyr Arg His Ile Thr Ile Ser Glu
 165 170 175

Ala Leu Glu Ala Ala Arg Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg
 180 185 190

Val Leu Ser Phe Gly Leu Glu Ala Gln Gln Gln His Val Ala Ala Pro
 195 200 205

MBI-0021.txt

Met Thr Pro Val Met Lys Leu Gln Glu Asp Gln Lys Val Ser Asn Gly
 210 215 220
 Ala Arg Asn Arg Phe His Gly Leu Ala Asp Gln Arg Leu Val Ala Arg
 225 230 235 240
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 245 250 255
 Asn Asn His Ser Val Asp Glu Ser Arg Ala Gln Ser Gly Ser Val Val
 260 265 270
 Glu Ala Gln Met Asn Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala
 275 280 285
 Cys Ile Pro Gly Val Pro Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro
 290 295 300
 Pro Pro Gly Phe Tyr Pro Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro
 305 310 315 320
 Tyr Trp Thr Ile Pro Met Leu Pro Pro His Gln Ser Ser Ser Pro Ile
 325 330 335
 Ser Gln Lys Cys Ser Asn Thr Asn Ser Pro Thr Leu Gly Lys His Pro
 340 345 350
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 355 360 365
 Lys Ala Gly Cys Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro
 370 375 380
 Asn Glu Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn
 385 390 395 400
 Glu Ala Met Cys Lys Ala Gly Gly Met Phe Lys Gly Phe Asp His Lys
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MBI-0021.txt

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 ttcaaatacca ataaagtttt aatttgatga agcttttttt aaaccatata atataaata 179
 atg ggt ggt cgt aaa cca tgt tgt gat gag gtt gga tta aga aag ggt 227
 Met Gly Gly Arg Lys Pro Cys Cys Asp Glu Val Gly Leu Arg Lys Gly
 1 5 10 15
 cca tgg aca gtg gaa gaa gat ggg aaa cta gtt gat ttc tta agg gca 275
 Pro Trp Thr Val Glu Glu Asp Gly Lys Leu Val Asp Phe Leu Arg Ala
 20 25 30
 cgt ggc aac tgc ggt ggt ggt gga gga gga tgg tgc tgg aga gac gtg 323
 Arg Gly Asn Cys Gly Gly Gly Gly Gly Gly Trp Cys Trp Arg Asp Val
 35 40 45
 cca aaa ctg gcg ggg cta agg agg tgt ggc aaa agt tgc cgt ctc cgg 371
 Pro Lys Leu Ala Gly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg
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 Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Leu Phe Thr Glu
 65 70 75 80
 gaa gaa atc caa cta gtc att gat ctt cat gct cgc ctt ggc aat aga 467
 Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg
 85 90 95
 tgg tcg aag att gca gtg gag tta cca gga aga aca gac aac gat atc 515
 Trp Ser Lys Ile Ala Val Glu Leu Pro Gly Arg Thr Asp Asn Asp Ile
 100 105 110
 aaa aat tat tgg aac act cat ata aag agg aag ctt ata aga atg ggt 563
 Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly
 115 120 125
 att gat cca aac aca cat cgt cga ttt gac caa caa aaa gtc aac gag 611
 Ile Asp Pro Asn Thr His Arg Arg Phe Asp Gln Gln Lys Val Asn Glu
 130 135 140
 gag gaa acg ata ttg gtc aac gat cca aag cct ctg tct gag acc gag 659
 Glu Glu Thr Ile Leu Val Asn Asp Pro Lys Pro Leu Ser Glu Thr Glu
 145 150 155 160
 gta tct gtt gct ttg aag aat gac acg tca gca gtg tta tca gga aat 707
 Val Ser Val Ala Leu Lys Asn Asp Thr Ser Ala Val Leu Ser Gly Asn
 165 170 175
 cta aac caa ttg gct gac gtg gac ggt gat gat cag ccg tgg agc ttt 755
 Leu Asn Gln Leu Ala Asp Val Asp Gly Asp Asp Gln Pro Trp Ser Phe

MBI-0021.txt

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195	200	205	
acg atg cta ttg tcc ggt gac att acg tca tca tgt tct tct tcg tca			851
Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser			
210	215	220	
tct ttg tgg atg aag tat gga gaa ttc gga tac gaa gat tta gaa ctt			899
Ser Leu Trp Met Lys Tyr Gly Glu Phe Gly Tyr Glu Asp Leu Glu Leu			
225	230	235	240
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Gly Cys Phe Asp Val			
245			
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gaatcaaagt tatgaaacat tgtaatttga tttccaaatt aatctaataa ataaatgtgc			1067
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Pro Lys Leu Ala Gly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg			
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Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Leu Phe Thr Glu			
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Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg			
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100	105	110	
Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly			
115	120	125	

MBI-0021.txt

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130 135 140

Glu Glu Thr Ile Leu Val Asn Asp Pro Lys Pro Leu Ser Glu Thr Glu
145 150 155 160

Val Ser Val Ala Leu Lys Asn Asp Thr Ser Ala Val Leu Ser Gly Asn
165 170 175

Leu Asn Gln Leu Ala Asp Val Asp Gly Asp Asp Gln Pro Trp Ser Phe
180 185 190

Leu Met Glu Asn Asp Glu Gly Gly Gly Gly Asp Ala Ala Gly Glu Leu
195 200 205

Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser
210 215 220

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Phe Asp Thr Gln Lys Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Gly
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Asp Asp Leu Phe Val His Gln Ser Ser Ile Arg Ser Glu Gly Phe Arg
35 40 45

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Ser Leu Ala Ala Glu Glu Ala Val Glu Phe Glu Val Glu Ile Asp Asn

MBI-0021.txt

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	70	75	80	
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	85	90	95	
ggt gga gga aga gga ggt gga cgc gga tct gga ggt gga tac ggc ggt	Gly Gly Gly Arg Gly Gly Gly Arg Gly Ser Gly Gly Gly Tyr Gly Gly			394
	100	105	110	
ggc ggt ggt gga tac gga gga aga gga ggt ggt ggt cga gga ggc agc	Gly Gly Gly Gly Tyr Gly Gly Arg Gly Gly Gly Gly Arg Gly Gly Ser			442
	115	120	125	
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	130	135	140	145
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	150	155	160	
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	165	170	175	
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	195	200		
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MBI-0021.txt

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 35 40 45

Arg Ser Leu Ala Ala Glu Glu Ala Val Glu Phe Glu Val Glu Ile Asp
 50 55 60

Asn Asn Asn Arg Pro Lys Ala Ile Asp Val Ser Gly Pro Asp Gly Ala
 65 70 75 80

Pro Val Gln Gly Asn Ser Gly Gly Gly Ser Ser Gly Gly Arg Gly Gly
 85 90 95

Phe Gly Gly Gly Arg Gly Gly Gly Arg Gly Ser Gly Gly Gly Tyr Gly
 100 105 110

Gly Gly Gly Gly Gly Tyr Gly Gly Arg Gly Gly Gly Gly Arg Gly Gly
 115 120 125

Ser Asp Cys Tyr Lys Cys Gly Glu Pro Gly His Met Ala Arg Asp Cys
 130 135 140

Ser Glu Gly Gly Gly Gly Tyr Gly Gly Gly Gly Gly Gly Gly Tyr Gly Gly
 145 150 155 160

Gly Gly Gly Tyr Gly Gly Gly Gly Gly Gly Tyr Gly Gly Gly Gly Arg
 165 170 175

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 <223> G562

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 ccttgaaacc attcct atg gga aat agc agc gag gaa cca aag cct cct acc 172
 Met Gly Asn Ser Ser Glu Glu Pro Lys Pro Pro Thr
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MBI-0021.txt

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Val	Tyr	Pro	Asp	Trp	Ala	Ala	Met	Gln	Ala	Tyr	Tyr	Gly	Pro	Arg	Val	
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Ala	Met	Pro	Pro	Tyr	Tyr	Asn	Ser	Ala	Met	Ala	Ala	Ser	Gly	His	Pro	
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Ala	Pro	Tyr	Ala	Ala	Val	Tyr	Pro	His	Gly	Gly	Gly	Val	Tyr	Ala	His	
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Pro	Gly	Ile	Pro	Met	Gly	Ser	Leu	Pro	Gln	Gly	Gln	Lys	Asp	Pro	Pro	
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Leu	Thr	Pro	Gly	Thr	Leu	Leu	Ser	Ile	Asp	Thr	Pro	Thr	Lys	Ser		
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Thr	Gly	Asn	Thr	Asp	Asn	Gly	Leu	Met	Lys	Lys	Leu	Lys	Glu	Phe	Asp	
		125			130					135					140	
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Glu	His	Lys	Arg	Ser	Arg	Asn	Ser	Ser	Glu	Thr	Asp	Gly	Ser	Thr	Asp	
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Gly	Ser	Asp	Gly	Asn	Thr	Thr	Gly	Ala	Asp	Glu	Pro	Lys	Leu	Lys	Arg	
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Ser	Arg	Glu	Gly	Thr	Pro	Thr	Lys	Asp	Gly	Lys	Gln	Leu	Val	Gln	Ala	
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Ser	Ser	Phe	His	Ser	Val	Ser	Pro	Ser	Ser	Gly	Asp	Thr	Gly	Val	Lys	
					210					215					220	
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Leu	Ile	Gln	Gly	Ser	Gly	Ala	Ile	Leu	Ser	Pro	Gly	Val	Ser	Ala	Asn	
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tcc	aac	ccc	ttc	atg	tca	caa	tct	tta	gcc	atg	gtt	cct	cct	gaa	act	892
Ser	Asn	Pro	Phe	Met	Ser	Gln	Ser	Leu	Ala	Met	Val	Pro	Pro	Glu	Thr	
			240					245					250			
tgg	ctt	cag	aac	gag	aga	gaa	ctg	aaa	cgg	gag	cga	agg	aaa	cag	tct	940

MBI-0021.txt

Trp	Leu	Gln	Asn	Glu	Arg	Glu	Leu	Lys	Arg	Glu	Arg	Lys	Gln	Ser		
	255						260					265				
aat	aga	gaa	tct	gct	aga	agg	tca	aga	tta	agg	aaa	cag	gcc	gag	aca	988
Asn	Arg	Glu	Ser	Ala	Arg	Arg	Ser	Arg	Leu	Arg	Lys	Gln	Ala	Glu	Thr	
	270					275					280					
gaa	gaa	ctt	gct	agg	aaa	gtg	gaa	gcc	ttg	aca	gcc	gaa	aac	atg	gca	1036
Glu	Glu	Leu	Ala	Arg	Lys	Val	Glu	Ala	Leu	Thr	Ala	Glu	Asn	Met	Ala	
	285				290					295					300	
tta	aga	tct	gaa	cta	aac	caa	ctt	aat	gag	aaa	tct	gat	aaa	cta	aga	1084
Leu	Arg	Ser	Glu	Leu	Asn	Gln	Leu	Asn	Glu	Lys	Ser	Asp	Lys	Leu	Arg	
				305					310					315		
gga	gca	aat	gca	acc	ttg	ttg	gac	aaa	ctg	aaa	tgc	tcg	gaa	ccc	gaa	1132
Gly	Ala	Asn	Ala	Thr	Leu	Leu	Asp	Lys	Leu	Lys	Cys	Ser	Glu	Pro	Glu	
				320				325					330			
aag	aga	gtc	ccc	gca	aat	atg	ttg	tct	aga	gtt	aag	aac	tca	gga	gct	1180
Lys	Arg	Val	Pro	Ala	Asn	Met	Leu	Ser	Arg	Val	Lys	Asn	Ser	Gly	Ala	
				335			340					345				
gga	gat	aag	aac	aag	aac	caa	gga	gac	aat	gat	tct	aac	tct	aca	agc	1228
Gly	Asp	Lys	Asn	Lys	Asn	Gln	Gly	Asp	Asn	Asp	Ser	Asn	Ser	Thr	Ser	
	350					355					360					
aaa	ttc	cat	caa	ctg	ctc	gat	acg	aag	cct	cga	gct	aaa	gca	gta	gct	1276
Lys	Phe	His	Gln	Leu	Leu	Asp	Thr	Lys	Pro	Arg	Ala	Lys	Ala	Val	Ala	
	365				370					375					380	
gca	ggc	tga	atcgatggta	attcatgtcg	atttctactt	aatttgtcga										1325
Ala	Gly															
cataa	acaaa	gaaaataagt	gctactaatt	tcagaaaaac	ttgatagata	gatagtatag										1385
tagagagaga	gagagagaga	gaggtgtgat	gattattgat	ctataaattt	tcggagagag											1445
agagggagaa	agagaaactt	ttcctccaga	tgaaaatttg	gtggttatgg	ttgttactgt											1505
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<213>	Arabidopsis thaliana															
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Pro	Ser	Ser	Pro	Pro	Val	Asp	Gln	Thr	Asn	Val	His	Val	Tyr	Pro	Asp	
			20					25					30			
Trp	Ala	Ala	Met	Gln	Ala	Tyr	Tyr	Gly	Pro	Arg	Val	Ala	Met	Pro	Pro	
	35						40					45				

MBI-0021.txt

Tyr Tyr Asn Ser Ala Met Ala Ala Ser Gly His Pro Pro Pro Tyr
 50 55 60

Met Trp Asn Pro Gln His Met Met Ser Pro Ser Gly Ala Pro Tyr Ala
 65 70 75 80

Ala Val Tyr Pro His Gly Gly Gly Val Tyr Ala His Pro Gly Ile Pro
 85 90 95

Met Gly Ser Leu Pro Gln Gly Gln Lys Asp Pro Pro Leu Thr Thr Pro
 100 105 110

Gly Thr Leu Leu Ser Ile Asp Thr Pro Thr Lys Ser Thr Gly Asn Thr
 115 120 125

Asp Asn Gly Leu Met Lys Lys Leu Lys Glu Phe Asp Gly Leu Ala Met
 130 135 140

Ser Leu Gly Asn Gly Asn Pro Glu Asn Gly Ala Asp Glu His Lys Arg
 145 150 155 160

Ser Arg Asn Ser Ser Glu Thr Asp Gly Ser Thr Asp Gly Ser Asp Gly
 165 170 175

Asn Thr Thr Gly Ala Asp Glu Pro Lys Leu Lys Arg Ser Arg Glu Gly
 180 185 190

Thr Pro Thr Lys Asp Gly Lys Gln Leu Val Gln Ala Ser Ser Phe His
 195 200 205

Ser Val Ser Pro Ser Ser Gly Asp Thr Gly Val Lys Leu Ile Gln Gly
 210 215 220

Ser Gly Ala Ile Leu Ser Pro Gly Val Ser Ala Asn Ser Asn Pro Phe
 225 230 235 240

Met Ser Gln Ser Leu Ala Met Val Pro Pro Glu Thr Trp Leu Gln Asn
 245 250 255

Glu Arg Glu Leu Lys Arg Glu Arg Arg Lys Gln Ser Asn Arg Glu Ser
 260 265 270

Ala Arg Arg Ser Arg Leu Arg Lys Gln Ala Glu Thr Glu Glu Leu Ala
 275 280 285

Arg Lys Val Glu Ala Leu Thr Ala Glu Asn Met Ala Leu Arg Ser Glu
 290 295 300

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Leu Asn Gln Leu Asn Glu Lys Ser Asp Lys Leu Arg Gly Ala Asn Ala
 305 310 315 320

Thr Leu Leu Asp Lys Leu Lys Cys Ser Glu Pro Glu Lys Arg Val Pro
 325 330 335

Ala Asn Met Leu Ser Arg Val Lys Asn Ser Gly Ala Gly Asp Lys Asn
 340 345 350

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 370 375 380

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 <223> G736

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 1 5 10 15
 gca ttt aac act cga aca ata aaa aat gaa gaa gag aca cac ccg ccg 96
 Ala Phe Asn Thr Arg Thr Ile Lys Asn Glu Glu Glu Thr His Pro Pro
 20 25 30
 gag caa gaa gcc aca ata gcc gtt aga tca tca tca tca tcg gat ctg 144
 Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu
 35 40 45
 acg gcc gag aag cgt ccg gat aag atc ata gca tgt cca aga tgc aag 192
 Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys
 50 55 60
 agc atg gag aca aag ttc tgt tac ttc aac aac tac aac ggt aat cag 240
 Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln
 65 70 75 80
 cct cga cac ttt tgt aaa ggc tgc cac cgt tac tgg acc gcc ggt ggt 288
 Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly
 85 90 95
 gca ctc cgg aac gtt ccc gtc ggc gcc ggt cgt cgg aag tcc aaa cca 336
 Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro
 100 105 110
 cct ggt cgt gtc gtg gtt ggt atg ctt gga gat gga aat ggt gtt cgc 384
 Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg

MBI-0021.txt

115	120	125	
caa gtc gag ctt ata aat ggc ttg ctc gtt gag gag tgg cag cat gcc			432
Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala			
130	135	140	
gca gcc gca gct cac ggt agt ttc cgg cat gat ttt ccc atg aag cgg			480
Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg			
145	150	155	160
ctc cgg tgt tac tcc gac ggt caa tcg tgc tga			513
Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys			
	165	170	

<210> 46
 <211> 170
 <212> PRT
 <213> Arabidopsis thaliana

<400> 46

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	20	25
Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu		
	35	40
Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys		
	50	55
Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln		
65	70	75
Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly		
	85	90
Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro		
	100	105
Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg		
	115	120
Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala		
	130	135
Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg		
145	150	155
Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys		

165

MBI-0021.txt
170

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 c atg gaa ctt aac aga tct gaa gca gac gaa gca aag gcc gag acc act 109
 Met Glu Leu Asn Arg Ser Glu Ala Asp Glu Ala Lys Ala Glu Thr Thr
 1 5 10 15
 ccc acc ggt gga gcc acc agc tca gcc aca gcc tct ggc tct tcc tcc 157
 Pro Thr Gly Gly Ala Thr Ser Ser Ala Thr Ala Ser Gly Ser Ser Ser
 20 25 30
 gga cgt cgt cca cgt ggt cgt cct gca ggt tcc aaa aac aaa ccc aaa 205
 Gly Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys
 35 40 45
 cct ccg acg att ata act aga gat agt cct aac gtc ctt aga tca cac 253
 Pro Pro Thr Ile Ile Thr Arg Asp Ser Pro Asn Val Leu Arg Ser His
 50 55 60
 gtt ctt gaa gtc acc tcc ggt tcg gac ata tcc gag gca gtc tcc acc 301
 Val Leu Glu Val Thr Ser Gly Ser Asp Ile Ser Glu Ala Val Ser Thr
 65 70 75 80
 tac gcc act cgt cgc ggc tgc ggc gtt tgc att ata agc ggc acg ggt 349
 Tyr Ala Thr Arg Arg Gly Cys Gly Val Cys Ile Ile Ser Gly Thr Gly
 85 90 95
 gcg gtc act aac gtc acg ata cgg caa cct gcg gct ccg gct ggt gga 397
 Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ala Pro Ala Gly Gly
 100 105 110
 ggt gtg att acc ctg cat ggt cgg ttt gac att ttg tct ttg acc ggt 445
 Gly Val Ile Thr Leu His Gly Arg Phe Asp Ile Leu Ser Leu Thr Gly
 115 120 125
 act gcg ctt cca ccg cct gca cca ccg gga gca gga ggt ttg acg gtg 493
 Thr Ala Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Thr Val
 130 135 140
 tat cta gcc gga ggt caa gga caa gtt gta gga ggg aat gtg gct ggt 541
 Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Asn Val Ala Gly
 145 150 155 160
 tcg tta att gct tcg gga ccg gta gtg ttg atg gct gct tct ttt gca 589
 Ser Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe Ala
 165 170 175
 aac gca gtt tat gat agg tta ccg att gaa gag gaa gaa acc cca ccg 637
 Asn Ala Val Tyr Asp Arg Leu Pro Ile Glu Glu Glu Glu Thr Pro Pro

MBI-0021.txt

180	185	190	
ccg aga acc acc ggg gtg cag cag cag cag ccg gag gcg tct cag tcg			685
Pro Arg Thr Thr Gly Val Gln Gln Gln Gln Pro Glu Ala Ser Gln Ser			
195	200	205	
tcg gag gtt acg ggg agt ggg gcc cag gcg tgt gag tca aac ctc caa			733
Ser Glu Val Thr Gly Ser Gly Ala Gln Ala Cys Glu Ser Asn Leu Gln			
210	215	220	
ggt gga aat ggt gga gga ggt gtt gct ttc tac aat ctt gga atg aat			781
Gly Gly Asn Gly Gly Gly Gly Val Ala Phe Tyr Asn Leu Gly Met Asn			
225	230	235	240
atg aac aat ttt caa ttc tcc ggg gga gat att tac ggt atg agc ggc			829
Met Asn Asn Phe Gln Phe Ser Gly Gly Asp Ile Tyr Gly Met Ser Gly			
245	250	255	
ggt agc gga gga ggt ggt ggc ggt gcg act aga ccc gcg ttt tag			874
Gly Ser Gly Gly Gly Gly Gly Gly Ala Thr Arg Pro Ala Phe			
260	265	270	
agtttttagcg ttttggtgac accttttggt gcgtttgcgt gtttgacctc aaactactag			934
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20	25	30	
Gly Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys			
35	40	45	
Pro Pro Thr Ile Ile Thr Arg Asp Ser Pro Asn Val Leu Arg Ser His			
50	55	60	
Val Leu Glu Val Thr Ser Gly Ser Asp Ile Ser Glu Ala Val Ser Thr			
65	70	75	80
Tyr Ala Thr Arg Arg Gly Cys Gly Val Cys Ile Ile Ser Gly Thr Gly			
85	90	95	
Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ala Pro Ala Gly Gly			
100	105	110	
Gly Val Ile Thr Leu His Gly Arg Phe Asp Ile Leu Ser Leu Thr Gly			

125

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MBI-0021.txt																
gtc	ccg	tcg	att	ctc	gcg	tta	gct	ttc	agc	atg	atc	cca	gaa	cga	agc	
Val	Pro	Ser	Ile	Leu	Ala	Leu	Ala	Phe	Ser	Met	Ile	Pro	Glu	Arg	Ser	193
			50					55					60			
cgt	aca	att	cac	gac	gtc	aat	cgc	gcg	tcg	caa	atc	acg	ctc	tct	tcg	241
Arg	Thr	Ile	His	Asp	Val	Asn	Arg	Ala	Ser	Gln	Ile	Thr	Leu	Ser	Ser	
		65					70					75				
ttg	aga	agc	agt	acc	aat	gct	tcg	tct	gtg	atg	gag	gag	gtc	gtg	gat	289
Leu	Arg	Ser	Ser	Thr	Asn	Ala	Ser	Ser	Val	Met	Glu	Glu	Val	Val	Asp	
	80					85					90					
cga	ggt	gaa	tcg	agt	ggt	cca	gga	tca	gat	ccg	aag	aaa	cag	aag	aaa	337
Arg	Val	Glu	Ser	Ser	Val	Pro	Gly	Ser	Asp	Pro	Lys	Lys	Gln	Lys	Lys	
95					100					105					110	
tcg	gat	ggt	ggt	gaa	gca	gcg	gcg	gtg	gag	gat	tcc	acg	gcg	gag	gaa	385
Ser	Asp	Gly	Gly	Glu	Ala	Ala	Ala	Val	Glu	Asp	Ser	Thr	Ala	Glu	Glu	
				115					120					125		
gga	gac	tcc	ggg	cct	gaa	gac	gcg	tct	ggg	aag	aca	tcg	aaa	cga	ccg	433
Gly	Asp	Ser	Gly	Pro	Glu	Asp	Ala	Ser	Gly	Lys	Thr	Ser	Lys	Arg	Pro	
			130					135					140			
cgt	tta	gtg	tgg	aca	ccg	cag	cta	cac	aag	aga	ttt	gtg	gac	gtt	gtg	481
Arg	Leu	Val	Trp	Thr	Pro	Gln	Leu	His	Lys	Arg	Phe	Val	Asp	Val	Val	
		145					150					155				
gct	cat	cta	ggg	att	aaa	aac	gca	gtg	ccg	aag	acg	att	atg	cag	ctg	529
Ala	His	Leu	Gly	Ile	Lys	Asn	Ala	Val	Pro	Lys	Thr	Ile	Met	Gln	Leu	
	160					165					170					
atg	aac	gtg	gaa	gga	ctt	act	cgt	gag	aac	gtt	gcg	tct	cat	ttg	cag	577
Met	Asn	Val	Glu	Gly	Leu	Thr	Arg	Glu	Asn	Val	Ala	Ser	His	Leu	Gln	
175					180					185					190	
aaa	tat	agg	ctt	tac	ctt	aaa	cgg	att	caa	gga	ttg	acg	acg	gaa	gaa	625
Lys	Tyr	Arg	Leu	Tyr	Leu	Lys	Arg	Ile	Gln	Gly	Leu	Thr	Thr	Glu	Glu	
			195						200					205		
gat	cct	tat	tcg	tcg	tcg	gat	cag	ctc	ttc	tct	tca	acg	ccg	gtt	cct	673
Asp	Pro	Tyr	Ser	Ser	Ser	Asp	Gln	Leu	Phe	Ser	Ser	Thr	Pro	Val	Pro	
			210					215					220			
cca	cag	agc	ttt	caa	gac	ggc	gga	gga	agt	aac	gga	aag	ttg	ggg	gtt	721
Pro	Gln	Ser	Phe	Gln	Asp	Gly	Gly	Gly	Ser	Asn	Gly	Lys	Leu	Gly	Val	
		225					230					235				
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Pro	Val	Pro	Val	Pro	Ser	Met	Val	Pro	Ile	Pro	Gly	Tyr	Gly	Asn	Gln	
	240					245					250					
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Met	Gly	Met	Gln	Gly	Tyr	Tyr	Gln	Gln	Tyr	Ser	Asn	His	Gly	Asn	Glu	
255					260					265					270	
tca	aac	caa	tat	atg	atg	cag	cag	aat	aag	ttt	gga	aca	atg	gtg	aca	865
Ser	Asn	Gln	Tyr	Met	Met	Gln	Gln	Asn	Lys	Phe	Gly	Thr	Met	Val	Thr	
				275					280					285		
tat	cct	tct	gtt	ggg	ggg	ggg	gac	gtg	aat	gac	aag	taa	atggatcctta			914
Tyr	Pro	Ser	Val	Gly	Gly	Gly	Asp	Val	Asn	Asp	Lys					
			290					295								

MBI-0021.txt

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aaggctata atttgctcta cagagagata ctgggtcttg gcttatgggt tattttccca 974
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ttgtatagaa aatgatttcg agaaaatcac tgggaagctt ggtattgttg gaggatgaag 1094
ccttctatga atgatttagt ttcctactgt ctccattctt tatgaggtaa taaagccttc 1154
ttttgctcat cgcttgtagt cttcttaaata tcaagacagc gtcacatgtt tggtcgggta 1214
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Asp Ala Gly Gly Gly Asp Glu Tyr Arg Ile Pro Glu Trp Glu Ile Gly
20 25 30

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Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu Val Pro
35 40 45

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Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser Arg Thr
50 55 60

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Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser Leu Arg
65 70 75 80

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Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp Arg Val
85 90 95

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Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys Ser Asp
100 105 110

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Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu Gly Asp
115 120 125

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Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro Arg Leu
130 135 140

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Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val Ala His
145 150 155 160

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Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu Met Asn
 165 170 175

Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln Lys Tyr
 180 185 190

Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu Asp Pro
 195 200 205

Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro Pro Gln
 210 215 220

Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val Pro Val
 225 230 235 240

Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln Met Gly
 245 250 255

Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu Ser Asn
 260 265 270

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 275 280 285

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 Asn Phe Leu Val Pro Phe Glu Glu Thr Asn Val Leu Thr Phe Phe Ser
 5 10 15

tct tct tct tcc tct tct ctt tct tct cct tct ttc ccc att cac aac 152
 Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His Asn
 20 25 30

tct tcc tcc act act act act cat gca cct cta ggg ttt tct aat aat 200
 Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn Asn
 35 40 45

MBI-0021.txt

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ctt cag ggt gga gga ccc ttg gga tca aag gtg gtt aat gat gat cag      248
Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp Gln
50                               55                               60                               65

gag aat ttt gga ggt gga act aac aat gat gct cat tct aat tct tgg      296
Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser Trp
70                               75                               80

tgg aga tca aat agt gga agt gga gat atg aag aac aaa gtg aag ata      344
Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys Ile
85                               90                               95

agg agg aaa cta aga gag cca aga ttc tgt ttc caa acc aaa agc gat      392
Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser Asp
100                              105                              110

gtt gat gtt ctt gac gat ggc tac aaa tgg cgt aaa tat ggt cag aaa      440
Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln Lys
115                              120                              125

gtc gtc aag aac agc ctt cac ccc agg agt tat tac aga tgc aca cac      488
Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr His
130                              135                              140                              145

aac aac tgt agg gtg aaa aag aga gtg gag cga cta tcg gaa gat tgt      536
Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp Cys
150                              155                              160

aga atg gtg att act act tac gaa ggt cgt cac aac cac att ccc tct      584
Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro Ser
165                              170                              175

gat gac tcc act tct cct gac cat gat tgt ctc tct tcc ttt taa      629
Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe
180                              185                              190

catctcttttc tatatatcta tatatagaca gttatatgtg cacatataga tgtgtgatat      689

attgcatatt tgatattgca tgtgttttttc aagagtatgt catcagatgt tatgcatata      749

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20                               25                               30

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Asn Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn
35                               40                               45

```

MBI-0021.txt

Asn Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp
50 55 60

Gln Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser
65 70 75 80

Trp Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys
85 90 95

Ile Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser
100 105 110

Asp Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln
115 120 125

Lys Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr
130 135 140

His Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp
145 150 155 160

Cys Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro
165 170 175

Ser Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe
180 185 190

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<212> DNA
<213> Arabidopsis thaliana

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<223> G592

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ttacaagaag agaaaacaga ggaaatttcg ttgcattttt tttacatatt gattcgatta 120
atg gat tca aat aat cat ctc tac gac ccg aat ccc acc ggg tcg ggt 168
Met Asp Ser Asn Asn His Leu Tyr Asp Pro Asn Pro Thr Gly Ser Gly
1 5 10 15
ctt ctt cgt ttt aga tca gct ccg agc tct gtt ctc gcc gct ttt gtt 216
Leu Leu Arg Phe Arg Ser Ala Pro Ser Ser Val Leu Ala Ala Phe Val
20 25 30
gac gac gac aag att ggt ttc gac tcc gat agg ttg ctt tca aga ttc 264
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MBI-0021.txt

Asp	Asp	Asp	Lys	Ile	Gly	Phe	Asp	Ser	Asp	Arg	Leu	Ser	Arg	Phe	
		35					40				45				
gtg	acc	tct	aat	ggc	gtt	aac	gga	gat	ctg	ggt	tca	cct	aaa	ttc	gag
Val	Thr	Ser	Asn	Gly	Val	Asn	Gly	Asp	Leu	Gly	Ser	Pro	Lys	Phe	Glu
	50					55				60					
gag	acc	tct	ccg	gtt	tcg	tta	acg	aac	acc	tct	gtt	tca	tac	gcc	gcc
Asp	Lys	Ser	Pro	Val	Ser	Leu	Thr	Asn	Thr	Ser	Val	Ser	Tyr	Ala	Ala
65				70					75					80	
act	ctg	ccg	cca	ccg	ccg	cag	ctt	gag	ccg	tcg	agt	ttt	ctg	ggg	ttg
Thr	Leu	Pro	Pro	Pro	Pro	Gln	Leu	Glu	Pro	Ser	Ser	Phe	Leu	Gly	Leu
				85					90				95		
ccg	ccg	cat	tac	ccg	agg	cag	agt	aaa	ggg	ata	atg	aac	tcg	gtt	ggg
Pro	Pro	His	Tyr	Pro	Arg	Gln	Ser	Lys	Gly	Ile	Met	Asn	Ser	Val	Gly
			100					105					110		
ttg	gat	cag	ttt	ctc	ggg	atc	aat	aat	cat	cac	acc	aaa	cca	gtt	gaa
Leu	Asp	Gln	Phe	Leu	Gly	Ile	Asn	Asn	His	His	Thr	Lys	Pro	Val	Glu
		115					120					125			
tct	aat	ctt	ctc	cgt	caa	agc	agc	tct	cca	gcc	gga	atg	ttt	act	aat
Ser	Asn	Leu	Leu	Arg	Gln	Ser	Ser	Ser	Pro	Ala	Gly	Met	Phe	Thr	Asn
	130					135					140				
ctc	tct	gac	caa	aac	ggg	tat	ggg	tca	atg	agg	aat	ttg	atg	aat	tac
Leu	Ser	Asp	Gln	Asn	Gly	Tyr	Gly	Ser	Met	Arg	Asn	Leu	Met	Asn	Tyr
	145				150					155					160
gaa	gaa	gat	gaa	gag	agt	cca	tct	aat	tcc	aat	gga	tta	aga	cgc	cat
Glu	Glu	Asp	Glu	Glu	Ser	Pro	Ser	Asn	Ser	Asn	Gly	Leu	Arg	Arg	His
				165					170					175	
tgc	agt	ctc	tct	tca	agg	cca	cct	tct	tca	ctt	gga	atg	ctt	tct	caa
Cys	Ser	Leu	Ser	Ser	Arg	Pro	Pro	Ser	Ser	Leu	Gly	Met	Leu	Ser	Gln
			180					185					190		
ata	cct	gaa	atc	gca	ccc	gaa	act	aat	ttt	cca	tat	agc	cat	tgg	aat
Ile	Pro	Glu	Ile	Ala	Pro	Glu	Thr	Asn	Phe	Pro	Tyr	Ser	His	Trp	Asn
		195					200					205			
gat	cca	tcc	agc	ttt	att	gat	aac	tta	tcc	tca	ctt	aaa	aga	gaa	gcc
Asp	Pro	Ser	Ser	Phe	Ile	Asp	Asn	Leu	Ser	Ser	Leu	Lys	Arg	Glu	Ala
	210					215					220				
gag	gac	gat	gga	aaa	ttg	ttt	ctc	gga	gct	cag	aac	gga	gag	tcc	ggg
Glu	Asp	Asp	Gly	Lys	Leu	Phe	Leu	Gly	Ala	Gln	Asn	Gly	Glu	Ser	Gly
	225				230				235					240	
aat	cgt	atg	cag	tta	ctg	tcg	cat	cat	ttg	agc	cta	cca	aag	tca	tca
Asn	Arg	Met	Gln	Leu	Leu	Ser	His	His	Leu	Ser	Leu	Pro	Lys	Ser	Ser
				245					250					255	
tcg	aca	gcc	tcg	gac	atg	gtt	tca	gtg	gat	aag	tat	ctt	cag	cta	caa
Ser	Thr	Ala	Ser	Asp	Met	Val	Ser	Val	Asp	Lys	Tyr	Leu	Gln	Leu	Gln
			260					265					270		
gat	tct	gtt	cct	tgt	aaa	atc	aga	gcc	aaa	cgt	ggg	tgc	gct	aca	cat
Asp	Ser	Val	Pro	Cys	Lys	Ile	Arg	Ala	Lys	Arg	Gly	Cys	Ala	Thr	His
		275					280					285			

MBI-0021.txt

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cct cga agc atc gct gaa cgg gta aga aga acg cgg ata agc gag cga      1032
Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Glu Arg
290                               295                               300

atg agg aag tta caa gag ctt gtt cct aac atg gac aag caa acc aac      1080
Met Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn
305                               310                               315                               320

act tcg gat atg ttg gat tta gct gtg gat tac atc aaa gat tta caa      1128
Thr Ser Asp Met Leu Asp Leu Ala Val Asp Tyr Ile Lys Asp Leu Gln
325                               330                               335

aga cag tat aag att tta aac gac aac aga gct aac tgt aag tgt atg      1176
Arg Gln Tyr Lys Ile Leu Asn Asp Asn Arg Ala Asn Cys Lys Cys Met
340                               345                               350

aac aag gag aag aag tca ata tag ggcgcaacaa agtgtgtagt agataggact      1230
Asn Lys Glu Lys Lys Ser Ile
355

aaaaagcagg gagaaggaca agaaagaaac aatgtcatgt ctgaatattt ttagccgaa      1290

acagacccaaa ttgtctatgt aagctctcga gaaaagcatc tgcttccaac aaaattctaa      1350

gtaataaaat agtactcgat ttgttcttat ttcattatta caatgcagaa tctactaatc      1410

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<213> Arabidopsis thaliana

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<400> 54

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Leu Leu Arg Phe Arg Ser Ala Pro Ser Ser Val Leu Ala Ala Phe Val
20          25          30

Asp Asp Asp Lys Ile Gly Phe Asp Ser Asp Arg Leu Leu Ser Arg Phe
35          40          45

Val Thr Ser Asn Gly Val Asn Gly Asp Leu Gly Ser Pro Lys Phe Glu
50          55          60

Asp Lys Ser Pro Val Ser Leu Thr Asn Thr Ser Val Ser Tyr Ala Ala
65          70          75          80

Thr Leu Pro Pro Pro Pro Gln Leu Glu Pro Ser Ser Phe Leu Gly Leu
85          90          95

Pro Pro His Tyr Pro Arg Gln Ser Lys Gly Ile Met Asn Ser Val Gly
100         105         110

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MBI-0021.txt

Leu Asp Gln Phe Leu Gly Ile Asn Asn His His Thr Lys Pro Val Glu
 115 120 125
 Ser Asn Leu Leu Arg Gln Ser Ser Ser Pro Ala Gly Met Phe Thr Asn
 130 135 140
 Leu Ser Asp Gln Asn Gly Tyr Gly Ser Met Arg Asn Leu Met Asn Tyr
 145 150 155 160
 Glu Glu Asp Glu Glu Ser Pro Ser Asn Ser Asn Gly Leu Arg Arg His
 165 170 175
 Cys Ser Leu Ser Ser Arg Pro Pro Ser Ser Leu Gly Met Leu Ser Gln
 180 185 190
 Ile Pro Glu Ile Ala Pro Glu Thr Asn Phe Pro Tyr Ser His Trp Asn
 195 200 205
 Asp Pro Ser Ser Phe Ile Asp Asn Leu Ser Ser Leu Lys Arg Glu Ala
 210 215 220
 Glu Asp Asp Gly Lys Leu Phe Leu Gly Ala Gln Asn Gly Glu Ser Gly
 225 230 235 240
 Asn Arg Met Gln Leu Leu Ser His His Leu Ser Leu Pro Lys Ser Ser
 245 250 255
 Ser Thr Ala Ser Asp Met Val Ser Val Asp Lys Tyr Leu Gln Leu Gln
 260 265 270
 Asp Ser Val Pro Cys Lys Ile Arg Ala Lys Arg Gly Cys Ala Thr His
 275 280 285
 Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Glu Arg
 290 295 300
 Met Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn
 305 310 315 320
 Thr Ser Asp Met Leu Asp Leu Ala Val Asp Tyr Ile Lys Asp Leu Gln
 325 330 335
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 340 345 350
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MBI-0021.txt

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aac aaa gga gct tgg act aaa gaa gaa gat caa cgt ctc gta gat tat 98
 Asn Lys Gly Ala Trp Thr Lys Glu Glu Asp Gln Arg Leu Val Asp Tyr
 15 20 25

atc cgt aat cac ggt gaa ggt tgt tgg cgt tct ctt cct aaa tcc gct 146
 Ile Arg Asn His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ser Ala
 30 35 40

gga ttg ttg cgt tgt ggt aaa agt tgt aga ttg aga tgg att aat tac 194
 Gly Leu Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr
 45 50 55 60

ctt cgt cct gat ctt aaa cgt ggt aat ttt act gat gat gaa gat caa 242
 Leu Arg Pro Asp Leu Lys Arg Gly Asn Phe Thr Asp Asp Glu Asp Gln
 65 70 75

atc atc atc aaa ctc cat agc tta ctc ggt aac aaa tgg tca ttg ata 290
 Ile Ile Ile Lys Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile
 80 85 90

gct gga aga tta cca gga aga aca gat aac gaa ata aag aat tat tgg 338
 Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp
 95 100 105

aac act cat att aag agg aag ctt ctt agt cac ggt att gat cca caa 386
 Asn Thr His Ile Lys Arg Lys Leu Leu Ser His Gly Ile Asp Pro Gln
 110 115 120

act cat cgt cag att aac gaa tcc aaa acg gtg tcg tct caa gtt gtt 434
 Thr His Arg Gln Ile Asn Glu Ser Lys Thr Val Ser Ser Gln Val Val
 125 130 135 140

gtt cct att caa aac gat gcc gtt gag tat tct ttt tcc aat tta gcc 482
 Val Pro Ile Gln Asn Asp Ala Val Glu Tyr Ser Phe Ser Asn Leu Ala
 145 150 155

gtt aaa ccg aag acg gaa aat tcc tcc gat aac gga gct tcg act agc 530
 Val Lys Pro Lys Thr Glu Asn Ser Ser Asp Asn Gly Ala Ser Thr Ser
 160 165 170

ggc acg acg acg gac gag gat ctc cgg cag aat ggg gag tgt tat tat 578
 Gly Thr Thr Asp Glu Asp Leu Arg Gln Asn Gly Glu Cys Tyr Tyr
 175 180 185

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MBI-0021.txt

Ser Asp Asn Ser Gly His Ile Lys Leu Asn Leu Asp Leu Thr Leu Gly
 190 195 200
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 Phe Gly Ser Trp Ser Gly Arg Ile Val Gly Val Gly Ser Ser Ala Asp
 205 210 215 220
 tct aaa ccg tgg tgc gac ccg gtg atg gag gcg cgt ttg tca ctg ttg 722
 Ser Lys Pro Trp Cys Asp Pro Val Met Glu Ala Arg Leu Ser Leu Leu
 225 230 235
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<210> 56
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 <213> Arabidopsis thaliana

<400> 56

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 Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ser Ala Gly Leu Leu Arg
 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60
 Leu Lys Arg Gly Asn Phe Thr Asp Asp Glu Asp Gln Ile Ile Ile Lys
 65 70 75 80
 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110
 Lys Arg Lys Leu Leu Ser His Gly Ile Asp Pro Gln Thr His Arg Gln
 115 120 125
 Ile Asn Glu Ser Lys Thr Val Ser Ser Gln Val Val Val Pro Ile Gln
 130 135 140
 Asn Asp Ala Val Glu Tyr Ser Phe Ser Asn Leu Ala Val Lys Pro Lys
 145 150 155 160
 Thr Glu Asn Ser Ser Asp Asn Gly Ala Ser Thr Ser Gly Thr Thr Thr
 165 170 175

MBI-0021.txt

Asp Glu Asp Leu Arg Gln Asn Gly Glu Cys Tyr Tyr Ser Asp Asn Ser
 180 185 190

Gly His Ile Lys Leu Asn Leu Asp Leu Thr Leu Gly Phe Gly Ser Trp
 195 200 205

Ser Gly Arg Ile Val Gly Val Gly Ser Ser Ala Asp Ser Lys Pro Trp
 210 215 220

Cys Asp Pro Val Met Glu Ala Arg Leu Ser Leu Leu
 225 230 235

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MBI-0021.txt

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